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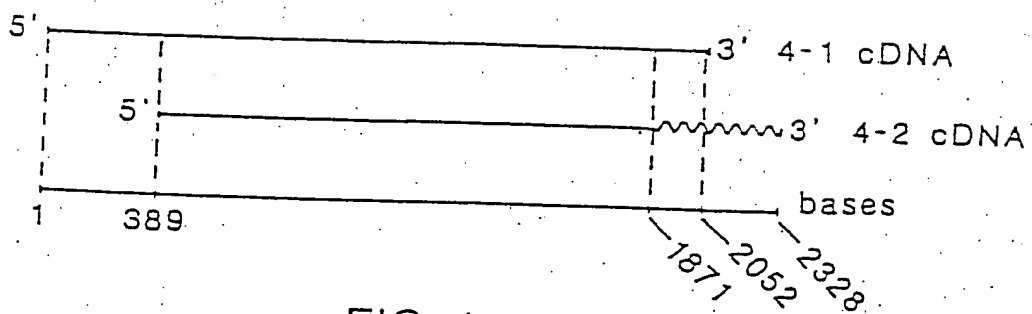


FIG. 1



GGC ACC GGG 10 GCG CCG CCG CCG CTG CTG CTA 30 CTG CCG CTG CTG CTG CTC CTA 50 GGG ACC GGC
Gly Thr Gly Ala Pro Pro Pro Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr Gly

CTC TTG CCT 70 GCT AGC AGC CAC ATA GAG ACC 90 CCG GCC CAT GCG GAG GAG 110 CCG CTC CTG AAG
Leu Leu Pro Ala Ser Ser His Ile Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys

AGA CTC TTC TCC 130 GGT TAC AAC AAG TGG TCT CCG CCA GTA GGC AAT ATC 170 TCA GAT GTG GTC
Arg Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val

CTC GTC CCG TTT 190 GGC TTG TCC ATT GCT CAG CTC ATT GAC GTG GAC 230 AAG AAC CAG ATG
Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met

ATG ACA ACC AAC 250 GTG TGG GTG AAG CAG GAG TGG CAC GAC TAC AAG CTG 290 TGG GAC CCT
Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp Pro

GGT GAC TAC GAG AAT 310 GTC ACC TCC ATC 330 CCG ATC CCC TCT GAA CTC ATC TGG AGG CCT GAC
Gly Asp Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp

ATC GTC CTC TAC AAC AAT 370 GCG GAT GGA GAC TTT GCA GTC ACC CAC CTG 410 ACC AAG GCC CAC
Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His

CTG TTC TAT GAC 430 GGA AGG GTG CAG TGG 450 ACA CCC CCA GCC ATC TAT AAG AGC TCC TGC AGC
Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser

ATC GAC GTC ACC TTC TTC CCC TTT GAC 510 CAG CAG AAC TGT ACC ATG AAG TTT GGA TCC TGG
Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Gly Ser Trp

ACC TAC GAC AAG GCC AAG ATT GAC TTA 570 GTG AGC ATT CAT AGC CGT GTG GAC CAA CTG GAC
Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp

TTC TGG GAA AGT 610 GGG GAG TGG GTC ATC 630 GTG GAT GCT GTG GGC ACC TAC AAC ACC AGG AAG
Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys

TAC GAG TGC TGT 670 GCC GAG ATC TAT CCT GAC ATC ACC TAT GCC TTC ATC ATC CGA CCG CTG
Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu

CCG CTA TTC TAC ACC ATC AAC CTC ATC ATC 730 CCG TGC CTG CTC ATC TCC TGT CTC ACC GTG
Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val

FIG. 2A



790 810 830
CTG GTC TTC TAT CTG CCT TCA GAG TGT GGC GAG AAG GTC ACA CTG TGC ATC TCG GTG CTG
Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu

850 870 890
CTT TCT CTC ACC GTC TTC CTG CTG CTC ATC ACC GAG ATC ATC CCG TCC ACC TCG CTG GTC
Leu Ser Leu Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val

910 930 950
ATC CCG CTC ATC GGC GAG TAC CTC CTC TTC ACC ATG ATC TTC GTC ACC CTC TCC ATC GTC
Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val

970 990 1010
ATC ACG GTC TTC GTG CTC AAT GTG CAC CAC CGC TCG CCA CGC ACA CAC ACG ATG CCC GCC
Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro Ala

1030 1050 1070
TGG GTG CGT AGA GTC TTC CTG GAC ATC GTG CCT CGC CTC CTC TTC ATG AAG CGC CCC TCT
Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser

1090 1110 1130
GTG GTC AAA GAC AAC TGC CGG AGA CTT ATT GAG TCC ATG CAC AAG ATG GCC AAC GCC CCC
Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro

1150 1170 1190
CGC TTC TGG CCA GAG CCT GTG GGC GAG CCC GGC ATC TTG AGT GAC ATC TGC AAC CAA GGT
Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Gln Gly

1210 1230 1250
CTG TCA CCT GCC CCA ACT TTC TGC AAC CCC ACG GAC ACA GCA GTC GAG ACC CAG CCT ACG
Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro Thr Asp Thr Ala Val Glu Thr Gln Pro Thr

1270 1290 1310
TGC AAG TCA CCC CCC CTT GAG GTC CCT GAC TTG AAG ACA TCA GAG GTT GAG AAG GCC AGT
Cys Arg Ser Pro Pro Leu Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser

1330 1350 1370
CCC TGT CCA TCG CCT GGC TCC TGT CCT CCA CCC AAG AGC AGC AGT GGG GCT CCA ATG CTC
Pro Cys Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro Met Leu

1390 1410 1430
ATC AAA GCC AGG TCC CTG AGT GTC CAG CAT GTG CCC AGC TCC CAA GAA GCA GAA GAT
Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala Ala Glu Asp

1450 1470 1490
GGC ATC CGC TGC CGG TCT CGG AGT ATC CAG TAC TGT GTT TCC CAA GAT GGA GCT GCC TCC
Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly Ala Ala Ser

1510 1530 1550
CTG GCT GAC AGC AAG CCC ACC AGC TCC CCG ACC TCC CTG AAG GCC CGT CCA TCC CAG CTT
Leu Ala Asp Ser Lys Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu

FIG. 2B



1570 1590 1610
CCC GTG TCA GAC CAG GCC TCT CCA TGC AAA TGC ACA TGC AAG GAA CCA TCT CCT GTG TCC
Pro Val Ser Asp Gln Ala Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser

1630 1650 1670
CCA GTC ACT GTG CAC AAG GCG GGA GGC ACC AAA GCA CCT CCC CAA CAC CTG CCC CTG TCA
Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His Leu Pro Leu Ser

1690 1710 1730
CCA GCC CTG ACA CGG GCA GTA GAA GGC GTC CAG TAC ATT GCA GAC CAC CTC AAG GCA GAA
Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp His Leu Lys Ala Glu

1750 1770 1790
GAC ACT GAC TTC TCG GTG AAG GAG GAC TGG AAA TAC GTG GCC ATG GTC ATT GAC CGA ATC
Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile

1810 1830 1850
TTC CTC TGG ATG TTC ATC ATT GTC TGC CTT CTG GGC ACT GTG GGA CTC TTC CTG CCT CCC
Phe Leu Trp Met Phe Ile Ile Val Cys Leu Lue Gly Thr Val Gly Leu Phe Leu Pro Pro

1870 1890 1917
TGG CTG GCT GCT TGC TGA TGGCTTCGACAGTGTCTCAGGCTCACGTCTCCTGCTGACTTTGTTTCCAG
Trp Leu Ala Ala Cys

1943 1969 1997
TTTCTTCTCCGACAAAGTTGGCCTCCCTTCATTTATTCCTGTTATTTTGGGCTTCGTGTTATTAATATCCTTCCCTGCC
TCTGTGGCGCATTGTAAGTTTAAAAATTAATAGACCAAAGCC...3'

4-2 cDNA: 3' end

1867 1884 1912
CCC TGG CTG GCT GGT ATG ATC TAG GGAGTGGTGGTGGCCAGCTCCACATCTCTGTAGGGCCATAC
Pro Trp Leu Ala Gly Met Ile

1937 1963 1991
GACTCGTCACTACCCACATCTTCCAAACCGGCTGACCATGAGACACCTAGGAGAGAGATGCTTCTTGGGAGATG
GAAATTGGCCCTGCTTCTAGTCAGACTATGCGGCTGGTTGGAGAGAAATGAGGGCTGATACAGTTGCAGGCCGAGTCCC

2016 2042 2070
CATTAAAGTTTCTCCAGAGCAAGTGGCAGTACTCCCTGACTTACAGACAGCACACCCCATCTGTGTACAGAGAATGA

2095 2121 2149
TCCCGAGTTGATCTCAGTTGTCTTTGAGGCCATGAAAAATTCATCCACCTTGAGGAACCCAGAGCTCTCATGCTGTGG

2174 2200 2228
GATCAATAAGACCAAGAACTCTCCACTGTGACTCTGTGTCACACCCCTCTCCCTCCCCAAGAAGTGGTCCCTCATCC

2253 2279 2307
CCCAATTC...3'

FIG. 2C

[illegible]

FIG. 3A

180 Asp Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys Tyr Glu Cys Cys 200
 GAC TTC TGG GAA AGT 540 GAG GAG TGG GTC ATC GTC GAT GCT GTG GGC ACC TAC AAC ACC AGG AAG TAC GAG TGC TGT GCC GAG ATC TAT CCT 600
 210 Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr ACC ATC AAT AAC CTC ATC ATC ATC CCG CTA TTC TAC 660
 GAC ATC ACC TAT GCC TTC 630
 240 Val Leu Val Phe Tyr Tyr Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr 260
 GTC CTC GTC TTC TAT 720 CCT TCA GAG TGT TGT GGC GAG AAG GTC ACA CTT GTC CTC ACC GTC TTC Phe Leu Leu Leu 780
 270 Ile Thr Glu Ile Ile Pro Glu Val Ile Pro Leu Ile Thr Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val 290
 ATC ACC GAG ATC ATC 810 TCC ACC TCG CTC GTC ATC CCG CTC ATC GGC GAG TAC TAC CTC CTC TTC ACC ATG ATC TTC GTC ACC CTT TCC ATC 870
 300 Val Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr Thr Met Pro Ala Trp Val Arg Arg Val Phe Leu Asp Ile 320
 GTC ATC ACC GTC TTC 900 CTC AAT GTG CAC CAC CAC CGC TCG CCA CGC ACA CAC CAC ACG ATG ATG CCC GCG TGG GTG CGT AGA GTC TTC CTT GAG ATC 960
 330 Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala 350
 GTC CCT CGC CTC CTC 990 ATG AAG CGC CCC TCT GTG GTC AAA GAC AAC TGC CGG AGA CTT ATT GAG TCC ATG CAC AAG ATG GCC AAC GCC 1050
 360 Pro Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Gln Gly Leu Ser Pro Ala Pro Thr Phe Cys Asn 380
 CCC CCT TTC TGG CCA GAG CCT GTG GGC GGC CCC GGC ATC TTG AGT GAC ATC TGC AAC CAA GGT CTG TCA CCT GCC CCA ACT TTC TGC AAC 1140
 390 Pro Thr Asp Thr Ala Val Glu Thr Gln Pro Thr Cys Arg Ser Pro Pro Glu Thr Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala 410
 CCC ACC GAG ACA GCA GTC 1170 GAG ACC CAG CCT ACG TGC AGG TCA CCC CCC CTT GAG GTC CCT GAG TTG AAG ACA TCA GAG GAT GAG AAG GCC 1230
 400 1200

FIG. 3B



420 Ser Pro Cys Pro Gly Ser Cys Pro Pro Lys Ser Ser 430
AGT CCC TGT CCA TCG CCT GGC TCC TGT CCA CCC CCA AGC AGC AGC AGC
1260
450 His Val Pro Ser Ser Lys Glu Ala Glu Asp Gly Ile Arg Cys 460
CAT GTG CCC AGC TCC CAA GAA GCA GCA GAA GAT GGC ATC CGC TGC TGC
1350
480 Ser Leu Ala Asp Ser Lys Pro Thr Ser Thr Ser Leu Lys Ala 490
TCC GTG GCT GAC AGC ACC ACC AGC TCC TCC TCC TCC TCC TCC TCC
1440
510 Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser Pro Val Thr Val 520
AAA TCC ACA TGC AGC GAA CCA TCT CCT GTG TCC CCA GTC ACT GTG
1530
540 Ser Pro Ala Leu Thr Arg Ala Val Glu Gly Val Glu Thr Tyr Ile Ala Asp 550
TCA CCA GCC CTG ACA CGG GCA GTA GAA GGC GTC CAG TAC TAC ATT GCA GAC
1620
570 Trp Lys Tyr Val Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met 580
TGG AAA TAC GTG GCC ATG ATG ATC TAG GAC CCA ATC TTC CTC TGG ATG
1710
600 Pro Trp Leu Ala Gly Met Ile 610
CCC TGG CTG GCT GGT ATG ATC TAG GAC CCA ATC TTC CTC TGG ATG
1800
ACACCTAGGAGAGATGCTTCTTGGGAGATGGAGTTGGCCCTGGTTCTAGTCAGACTATGGCGGTGGTGGAGAGAAATGAGGGCTGATACAGTTGCAGGCCGAGTCCCCATT
1920 1950 1980 2010

FIG. 3C

FIG. 4A



ALPHA4 F V L N V H Y R S P R T H T M P A W V R R V F L D I V
ALPHA3 F V L N V H Y R T P T T H T M P T W V K A V F L N L L
ALPHA1 I V I N T H Y R S P S T H I M P E W V R K V F I D T I
----->

ALPHA4 P R L L F - - - M K R P S V V K D N C R R L I E S M H
ALPHA3 P R V M F - - - M T R P T S G E G D T P K T - - - -
ALPHA1 P N I M F F S T M K R P S R D K Q E K R I F - - - -

ALPHA4 X M A N A P R F W P E P V G E P G I L S D I C H O G L
ALPHA3 - - - - - - - - - - R T F Y G A E L S N L N C F S R
ALPHA1 - - - - - - - - - - T E D I D I S D I S G X P G

ALPHA4 S P A P T F C N P T D T A V E T Q P T C R S P P L E V
ALPHA3 A D S X S C K E G Y P C O D G T C C Y C H H R R V K I
ALPHA1 P P P M G F H - - - - - - - - - - - - - - - - - -

ALPHA4 P D L K T S E V E K A S P C P S P G S C P P P K S S S S
ALPHA3 S N F - - - - - - - - - - - - - - - - S A N L T R S S S S
ALPHA1 -

ALPHA4 G A P M L I K A R S L S V Q W V P S S Q E A A E D G I
ALPHA3 S E S V -
ALPHA1 -

ALPHA4 R C R S R S I O Y C V S Q D G A A S L A D S K P T S S
ALPHA3 -
ALPHA1 -

ALPHA4 P T S L X A R P S Q L P V S D Q A S P C X C T C K E P
ALPHA3 -
ALPHA1 -

ALPHA4 S P V S P V T V L K A G G T X A P P Q H L P L S P A L
ALPHA3 - - - - - - - - - - - - - - - - N A V L S L S A L S P E I
ALPHA1 - - - - - - - - - - - - - - - - - S P L I X H P E V
-----<

ALPHA4 T R A V E G V O Y I A D H L K A E D T D F S V K E D W
ALPHA3 K E A I O S V X Y I A E N M K A Q N V A K E I O D D W
ALPHA1 K S A I E G V X Y I A E T M K S D Q E S N N A A E E W
-->phipathic helix----->

ALPHA4 K Y V A M V I D R I F L W M F I I V C L L G T V G L F
ALPHA3 X Y V A M V I D R I F L W V F I L V C I L G T A G L F
ALPHA1 X Y V A M V M D H I L L G V F M L V C L I G T L A V F
-----<MSR IV----->

ALPHA4 L P P W L A G M I
ALPHA3 L O P L M A - R D D T
ALPHA1 A G R L I E L H Q Q G
-->

FIG. 4B

FIG. 5A

Clone 4-1;
Antisense

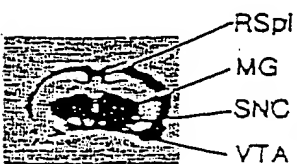
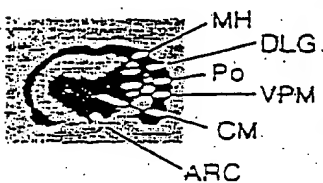
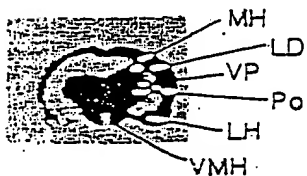
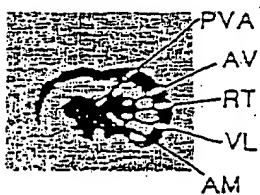
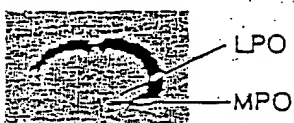
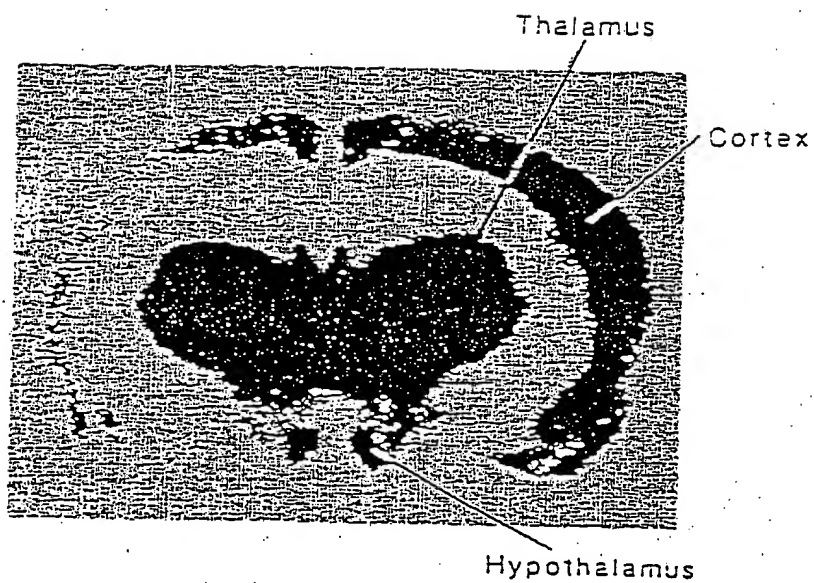


FIG. 5B

Clone 4-1;
Sense

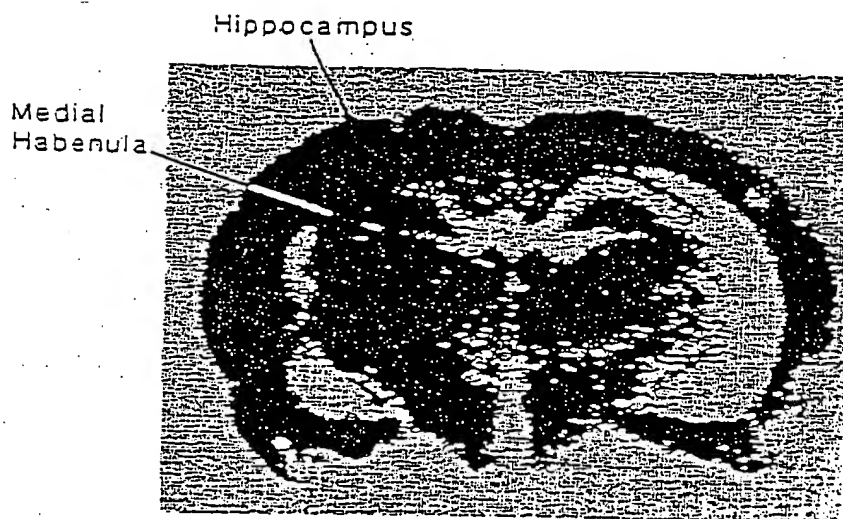


FIG. 6A



PROBE: Alpha 4

FIG. 6B



PROBE: Alpha 3

FIG. 7A

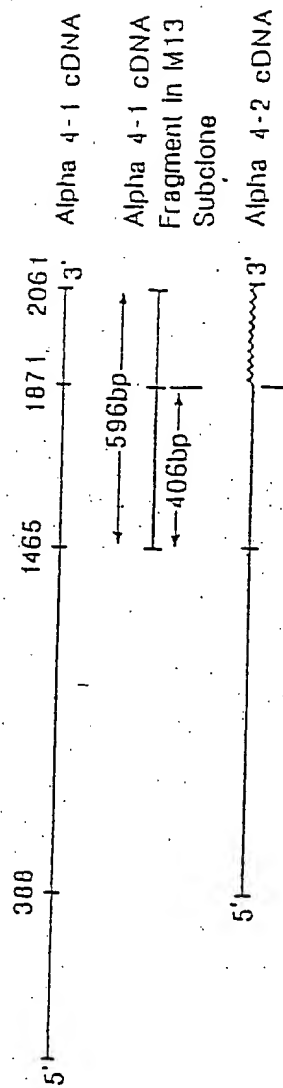


FIG. 7B

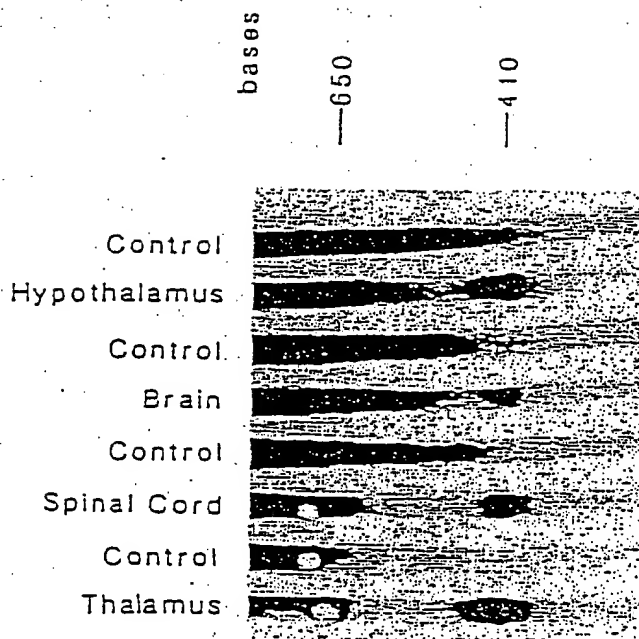
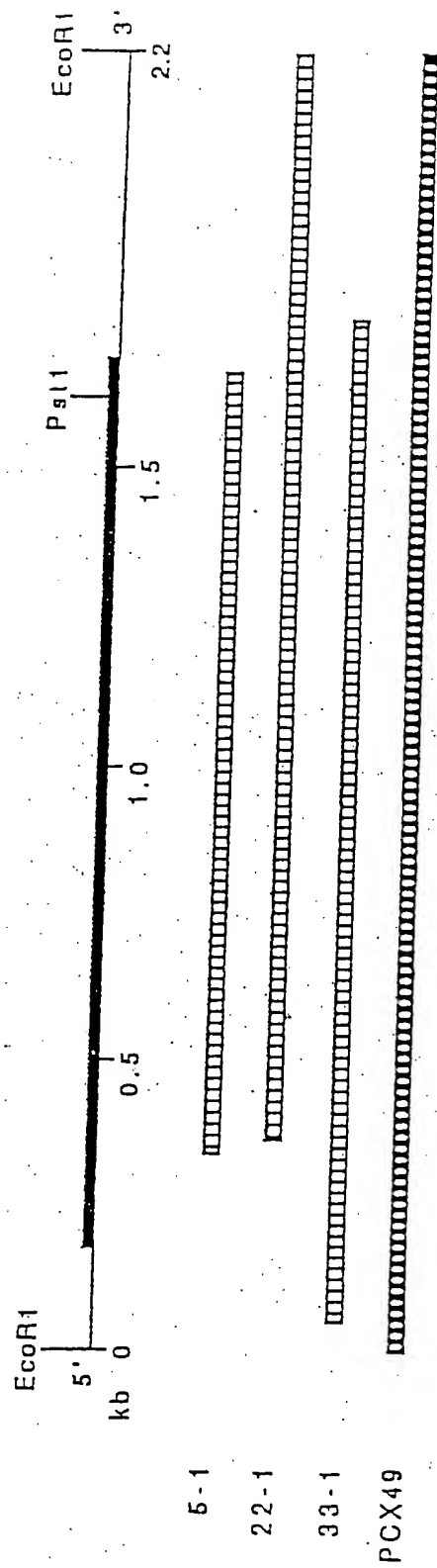


FIG. 8





5' -179
GGGGAACACACCCGGGACCGGCAAGAGCCGGGACCTCCCTCGTTGACAGGAACCTGCCCGTTTCAGTGAGCACCTTTAGACC -100
TGGAGGGCCGCGAGCCACCCCGGAGCAGGGGCTGCGGGCTTCAGCACCCAGCGCTCGACCCCGAGCCCTAGTATCCGAGAGGCTGCGCGCT -1
ATG CTG GCT TGC ATG GCC GGG CAC TCC AAC TCA ATG GCG CTG TTC AGC TTC AGC CTT CTT TGG CTG TGC TCA GGG
Met Leu Ala Cys Met Ala Gly His Ser Asn Ser Met Ala Leu Phe Ser Phe Ser Leu Leu Trp Leu Cys Ser Gly
1
GTT TTG GGA ACT GAC ACA GAG GAG GCG CTA GTG GAG CAT CTC TTA GAT CCC TCC CGC TAT AAC AAG CTG ATT CGT
Val Leu Gly Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg
26
CCA GCT ACT AAC GGC ICT GAG CTG GTG ACT GTA CAG CTC ATG GTA TCA TTG GCT CAG CTC ATT AGT GTG CAC GAG
Pro Ala Thr Asn Gly Ser Glu Leu Val Thr Val Gln Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu
51
GGG GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT TAC CCG CTC ACA TGG AAG CCT GAG
Arg Glu Gln Ile Met Thr Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp Tyr Arg Leu Thr Trp Lys Pro Glu
76
GAC TTC GAC AAT ATG AAG AAA GTC CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GIG GTT CTA TAC AAC AAT
Asp Phe Asp Asn Met Lys Lys Val Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn Asn
101
GCT GAC GGC ATG TAC GAA GTC TCC TTC TAT TCC AAT GCT GTG GTC TCC TAT GAT GGC AGC ATC TTT TGG CTA CCA
Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro
126
CCT GCC ATC TAC AAG AGT GCA TGC AAG ATT GAG GTG AAG CAC TTC CCA TTT GAC CAG AAT TGC ACC ATG AAG
Pro Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys
151

FIG. 9A



540
TTC CGC TCA TGG ACC TAC GAC CGT ACT GAG ATT GAC CTG GTG CTC AAA AGT GAT GTG GCC AGT CTG GAT GAC TTC 600
Phe Arg Ser Trp Thr Thr Tyr Asp Arg Thr Glu Ile Asp Leu Val Leu Lys Ser Asp Val Ala Ser Leu Asp Phe
176

630
ACA CCC AGC GGG GAG TGG GAC ATC ATC GCA CTG CCA GGC CGA CGC AAC GAG AAC CCA GAC GAC TCC ACC TAT GTG
Thr Pro Ser Gly Glu Thr Ile Ile Ala Leu Pro Gly Arg Arg Arg Asn Glu Asn Pro Asp Ser Thr Tyr Val
201

690
GAC ATC ACC TAT GAC TTC ATC ATT CGT CGC AAA CCA CTC TTC TAC ACT ATC AAC CTC ATC CCC TGC GTA CTC 750
Asp Ile Thr Tyr Asp Phe Ile Ile Arg Arg Lys Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Val Leu
226

780
ATC ACC TCG CTG GCC ATC CTG GTC TTC TAC CTG CCC TCA GAC TGT GGT GAA AAG ATG ACA CTT TGT ATT TCT GTG
Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Thr Leu Cys Ile Ser Val
251

840
CTG CTA GCA CTC ACG GTG TTC CTG CTG ATC TCC AAG ATT GTG CCT CCC ACC TCC CTC GAT GTA CCG CTG CTC GTG 900
Leu Leu Ala Leu Thr Thr Val Phe Leu Leu Leu Ile Ser Lys Ile Val Val Pro Thr Ser Leu Asp Val Pro Leu Val
276

930
GGC AAG TAC CTC ATG TTT ACC ATG GTG CTA GTC ACC TTC TCC ATC GTC ACC AGC GTG TGT GTG CTC AAT GTG CAC
Gly Lys Tyr Leu Met Phe Thr Thr His Thr Met Ala Pro Trp Val Lys Val Val Phe Leu Glu Lys Leu Pro Thr Leu Leu
301

990
CAC CGC TCG CCT ACC ACG CAC ACC ATG GCC CCC TGG GTC AAG GTG GTC TTC CTG GAG AAG CTG CCC ACC CTG CTC 1050
His Arg Ser Pro Thr Thr Thr His Thr Met Ala Pro Trp Val Lys Val Val Phe Leu Glu Lys Leu Pro Thr Leu Leu
326

1080
TTC CTG CAG CAG CCA CGC CAC CGC TGT GCA CGT CAG CGT CTG CGC TTG AGG AGG CGC CAG CGA GAG CGT GAG GGC
Phe Leu Gln Gln Pro Arg Arg His Arg Cys Ala Arg Gln Arg Leu Arg Arg Arg Gln Arg Gln Arg Glu Arg Glu Gly
351

FIG. 9B



GAG GCG GTT TTC TTC CGT GAA GGT CCT GCG GCT GAC CCA TGT ACC TGC TTT GTC AAC CCT GCA TCA GTG CAG GGC 1200
Glu Ala Val Phe Phe Arg Glu Gly Pro Ala Ala Asp Pro Cys Thr Cys Phe Val Asn Pro Ala Ser Val Gln Gly
376 1140 1170

TTG GCT GGG GCT TTC CGA GCT GAG CCC ACT GCA GCC GGC CCG GGG GGC TCT GTG GGG CCA TGC AGC TGT GGC CTC 1260
Leu Ala Gly Ala Phe Arg Ala Glu Pro Thr Ala Ala Gly Pro Gly Arg Ser Val Gly Pro Cys Ser Cys Gly Leu
401 1230 1260

GCG GAA GCA GTG GAT GGC GTA CGC TTC ATT GCG GAC CAC ATG CGA AGT GAG GAT GAT GAC CAG AGT GTG AGG GAG 1350
Arg Glu Ala Val Asp Gly Val Arg Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Arg Glu
426 1290 1320

GAC TGG AAA TAC GTT GCC ATG GTG ATC GAC CGC CTG TTC CTG TGG ATC TTT GTC TTT GTC TGT GGC ACC 1410
Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Leu Trp Ile Phe Val Phe Val Cys Val Phe Gly Thr
451 1380 1410

GTC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACT GCC ACT ACC TTC CTC CAC CCT GAC CAC TCA GCT CCC 1500
Val Gly Met Phe Leu Gln Pro Leu Phe Gln Asn Tyr Thr Ala Thr Thr Phe Leu His Pro Asp His Ser Ala Pro
476 1440 1470

AGC TCC AAG TGAGGTCTCATTCATTGTCAGCTCTCTACCCCGTGACCCCTGCGGTTTCAGTACTGGGTGCAAGATGGATCTCTCCCCACTCCACTGA 1596
Ser Ser Lys

AGCCTGCTTCACACCTCCGTTACACATAGTCTCTCCAGCCCTGGAGGCTGGACCCGCTGCCCTTGTGGTCGAGCCCTCTCCCTCTGAGCTCGTTCA 1695
GGCAGGAGTGCCCATGTTGGGGGCCACGGCTGGTAAGTAGAGGCCAGAGATCACAGAGCCACCTACCCCGATGAGGTGCTGGAGAGGCGCCAAAGAAAG 1794
AGACAGAGTTATCTGTGACCTCCAAAGTCATCGGAGAGGAGGAGGTAGGATAAGGGGCTCAGACTCTGGCAGAGTGGCGCTAGTACTTGGCGCCCAACCCA 1893
CTTAAGTGAGCGACACTGGTCTGGGAGGACTCGAAGTGTGGGAGCTCTCTTGGGAGCTCGGTCTCCCAACCCCTGTACCTCAGAGGGGCTCCAGACCCCGG 1992
GCTTCAGGTTCCCTTCTGCCAGTGC.....3'

FIG. 9C

NEURONIAL AND MUSCLE NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNITS

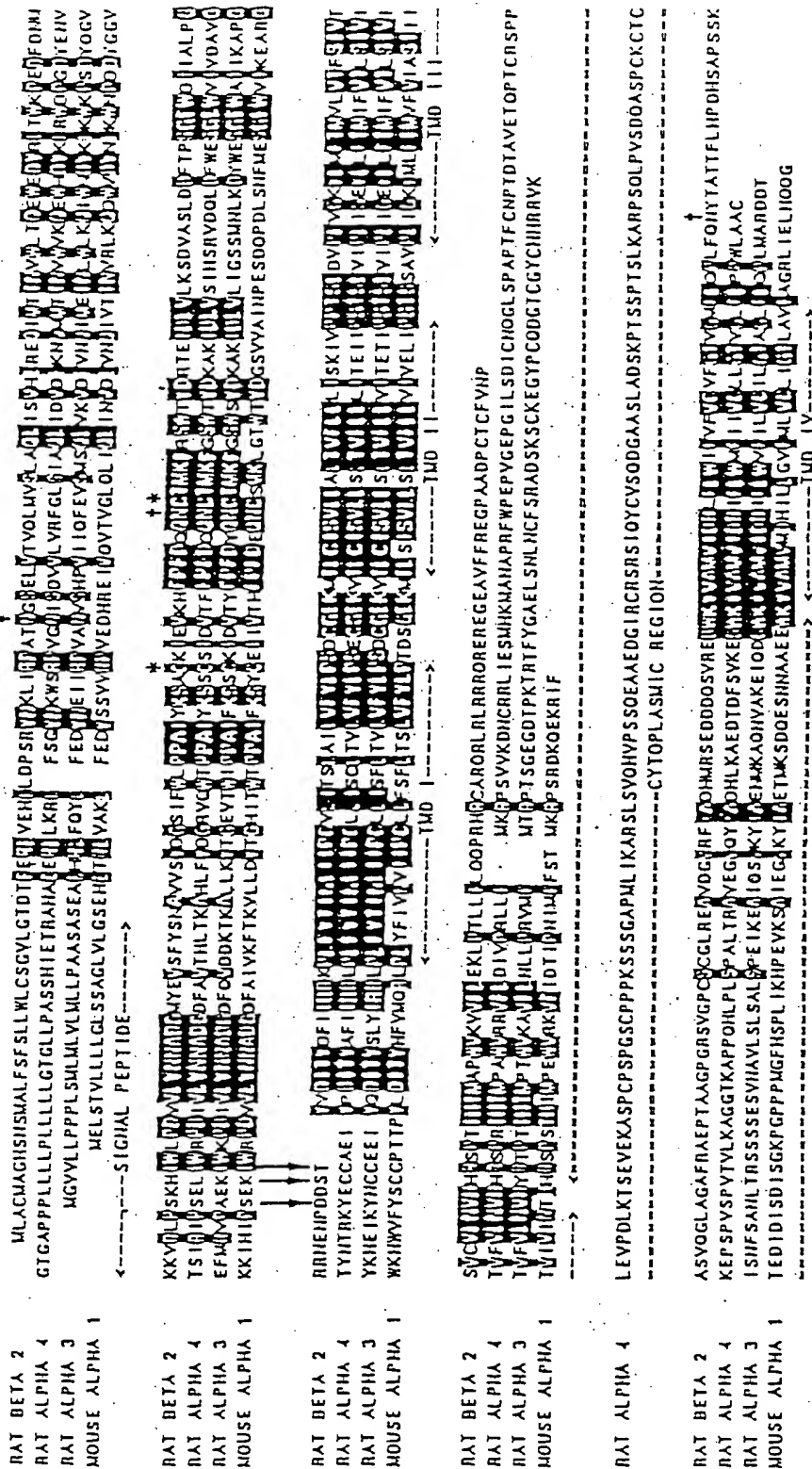


FIG. 10

FIG. 11A

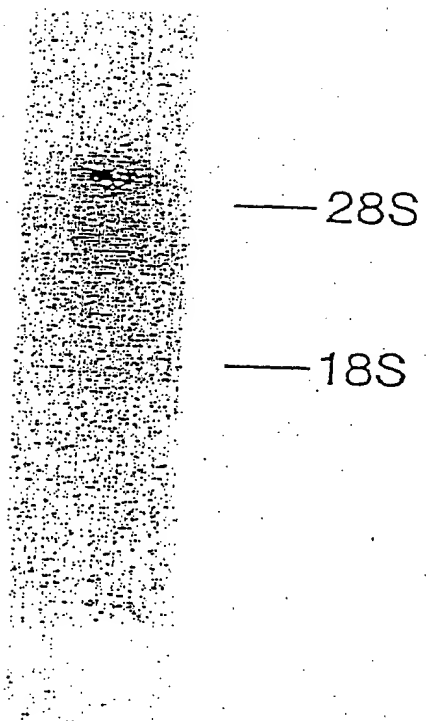


FIG. 11B

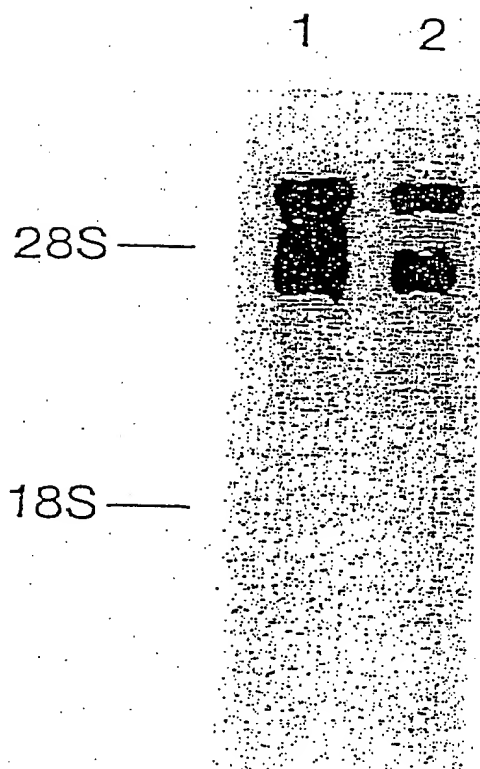


FIG. 12A

ANTISENSE

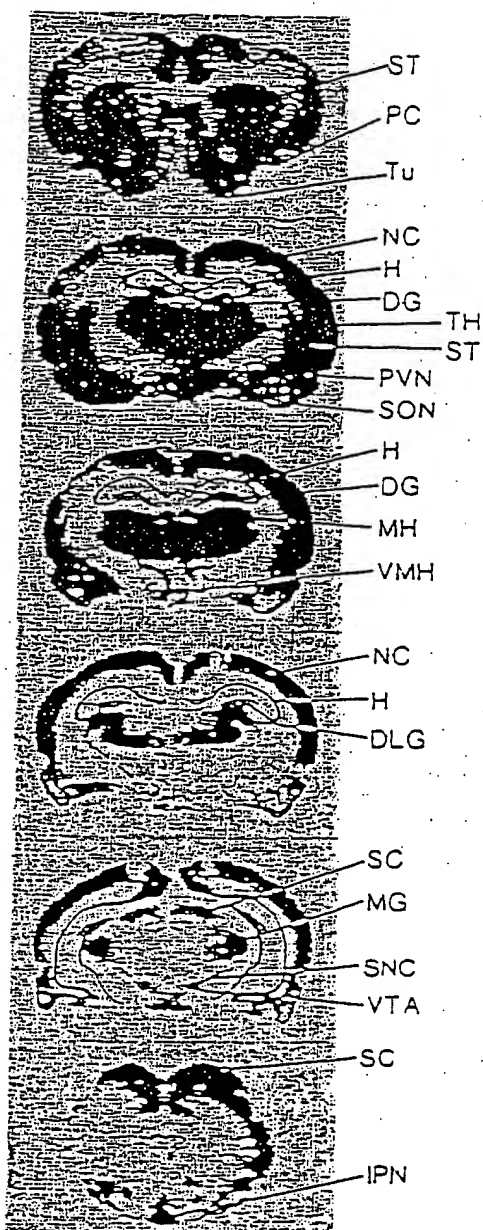
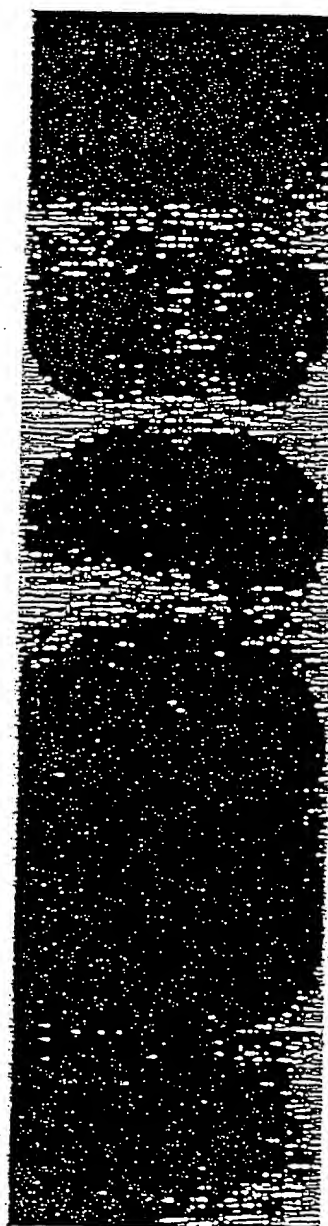


FIG. 12B

SENSE



[illegible]

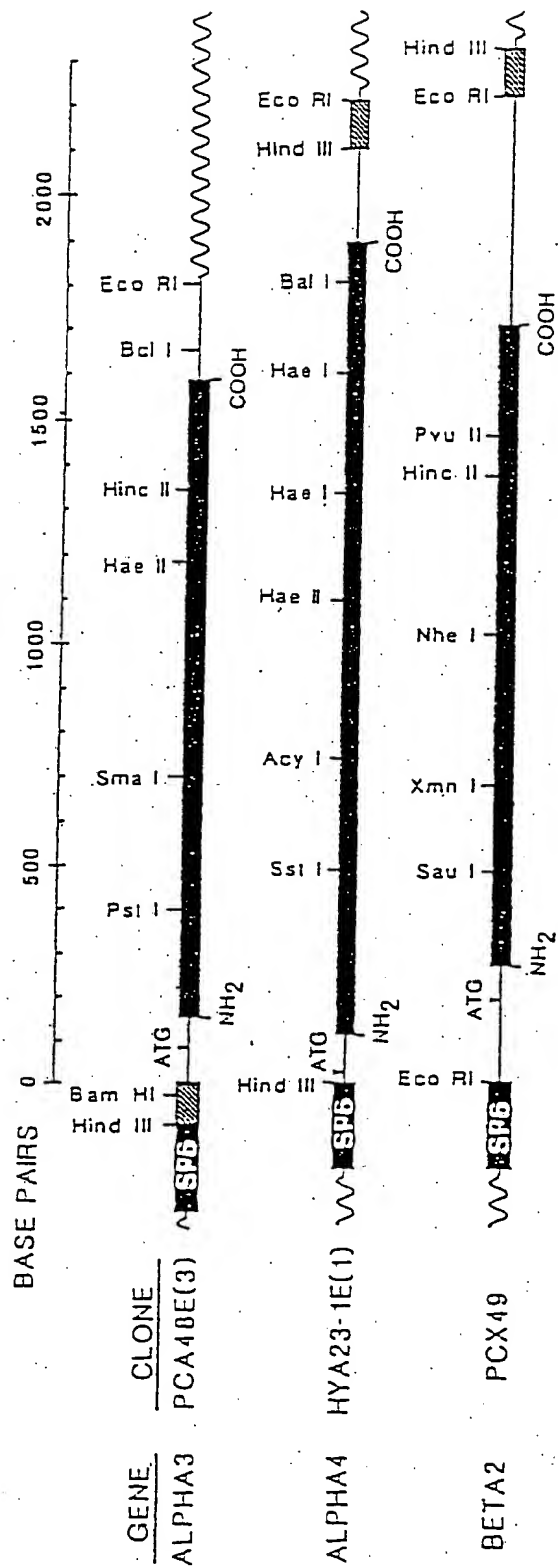


FIG. 14

mRNAs injected	Responses to Acetylcholine (ACh)	Responses to Nicotine (Nic)
----------------	----------------------------------	-----------------------------

FIG. 15A

alpha3
+ beta2

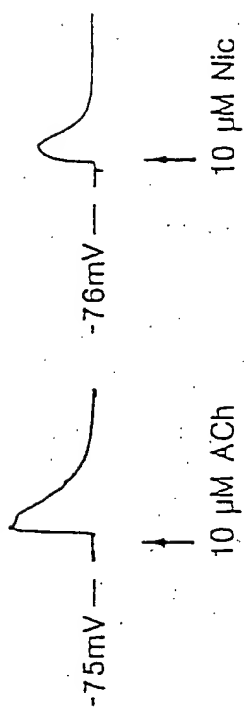


FIG. 15B

alpha4
+ beta2

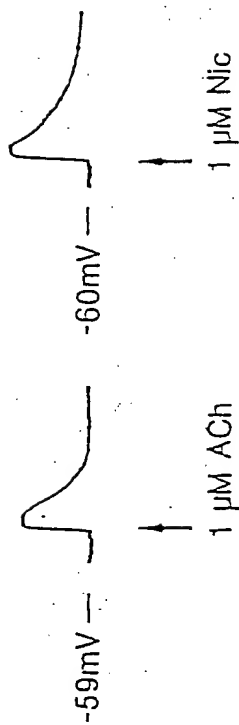


FIG. 15C

alpha4



FIG. 16A

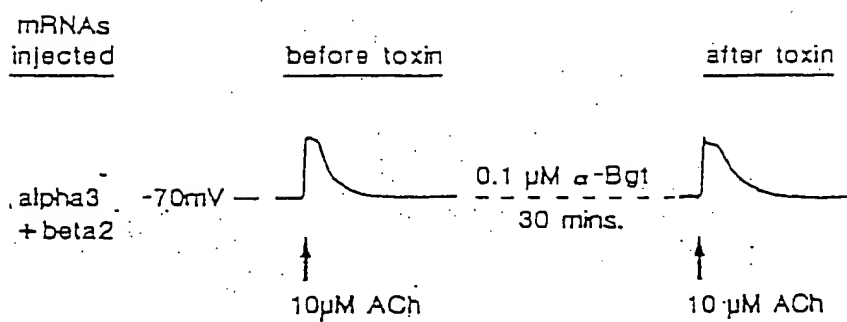


FIG. 16B

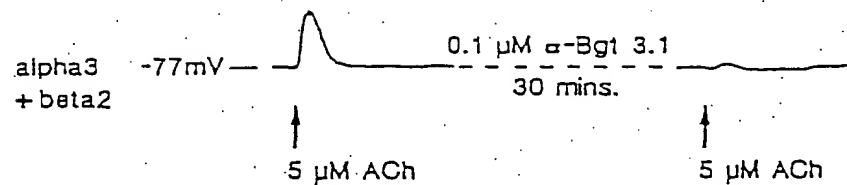


FIG. 16C

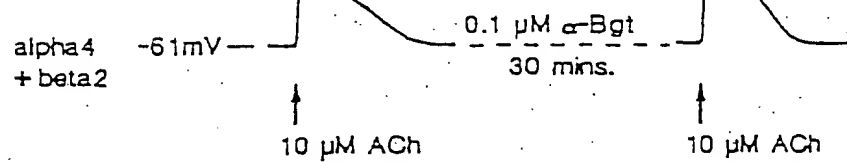
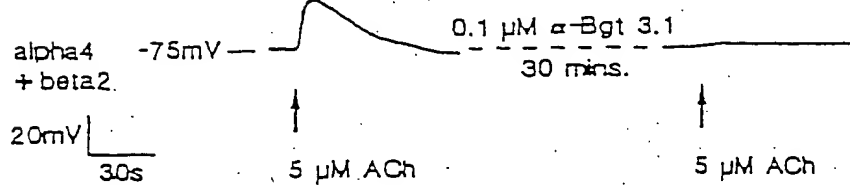


FIG. 16D



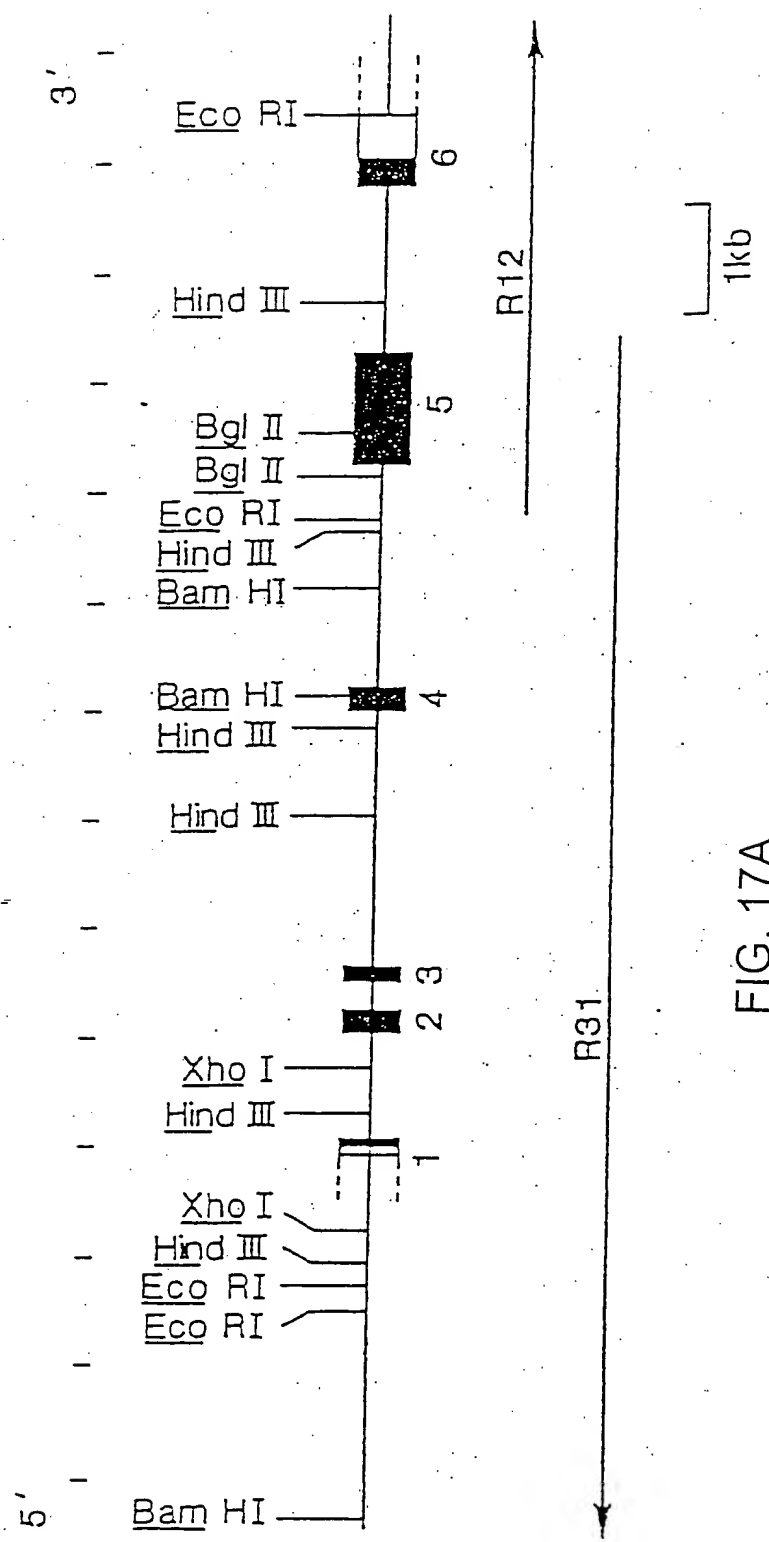
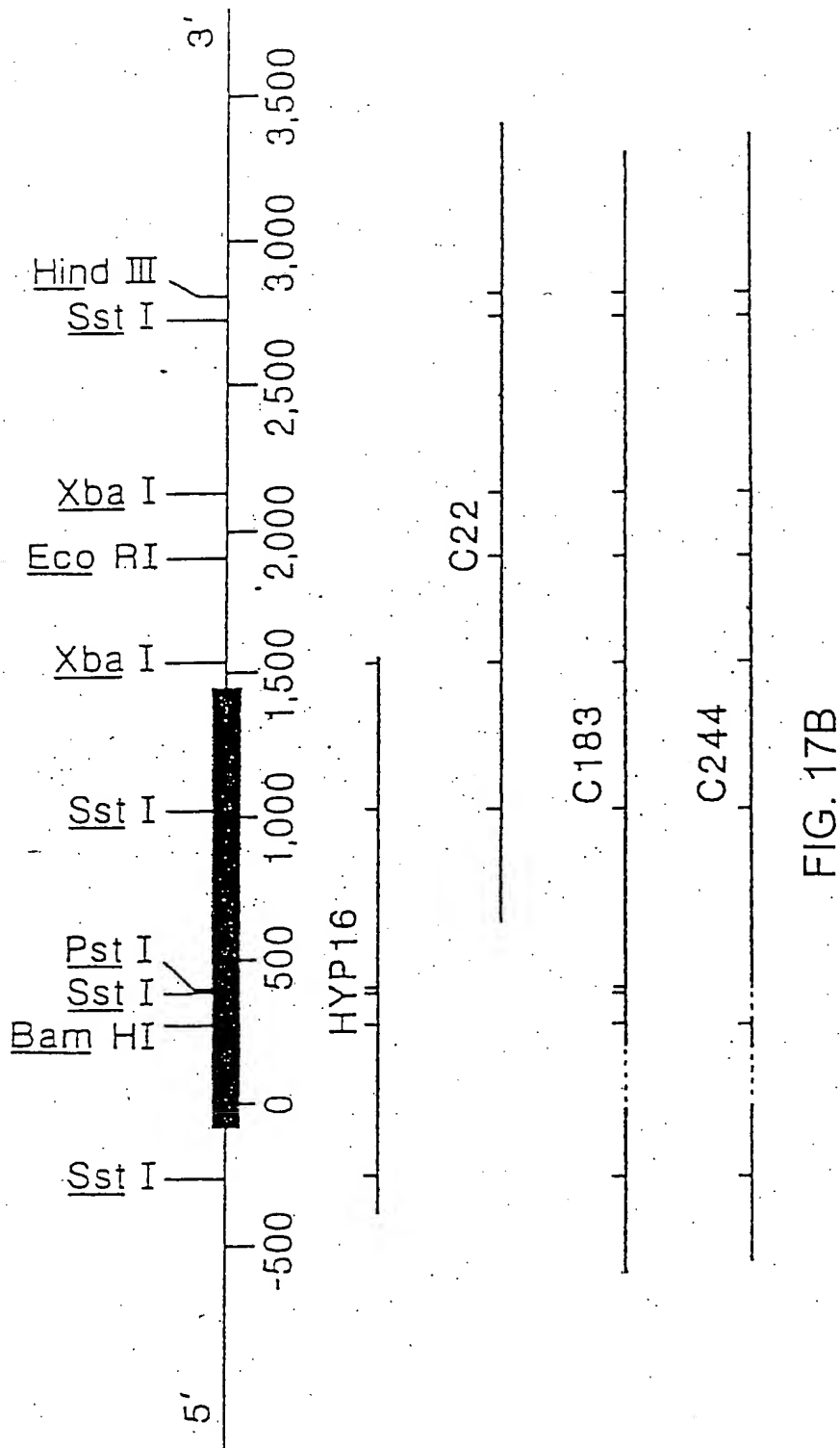


FIG. 17A



5'ACTGAGCATTC
 -360
 TGTGAACCTGGATCACCCTATCTCCAGGAGCTAGCTGATCCCTCATCCCAACAGTGCCCTCCCAACCTTGCAGGTCTGTGTCTGGGCAACATGAGCTGAGCTCTG
 -270
 TTCTGCACCTGTGCTCTCCAGGACCCCTCGTCAGCCACCCAGGTCTCCAGCGGTTGGTTCTCTGCATCCCTTGCAGGGGCTGTCTTCTATGACAATTGCAGAGAGACAGT
 -150
 GCCTCAAGAGCCAGCTCTTGGTAGTCCAGGGAACCCCTCTGAAGCC ATG ACC CTT TCC CAT TCT GCT CTC CAG TTC TGG ACA CAT CTT TAT CTC
 -60
 Met Thr Leu Ser His Ser Ala Leu Gln Phe Thr Trp His Leu Tyr Leu
 -20
 -30
 TGG TGT CTC CTT CTG GTG CCA G G gtgagt.....tatccccacag TG TTG ACC CAG CAA GGC TCA CAC ACC CAT GCT GAG GAC CGC CTG TTC
 Trp Cys Leu Leu Val Pro Ala V al Leu Thr Gln Gln Gly Ser His Thr His Ala Glu Asp Arg Leu Phe
 -10
 60
 AAA CAC CTG TTT GGA GGC TAC AAT CGC TGG GCA CGG CCA GTG CCC AAC ACT TCT GAT GTG GTG ATC GTG CGC TTT GGA TTA TCC ATT GCT
 Lys His Leu Phe Gly Gly Tyr Asn Arg Trp Ala Arg Pro Val Pro Asn Thr Ser Asp Val Ile Val Arg Phe Gly Leu Ser Ile Ala
 20
 90
 CAG CTC ATA GAT GTG gtgggc.....gctacaacag CAT GAG AAG AAT CAA ATG ATG ACC AAT GTC TGG CTA AAG CAG gtaaac.....
 Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Thr Thr Thr Asn Val Trp Leu Lys Gln
 50
 150
ccctaagcag GAA TGG AAT GAC TAC AAG CTG CGC TGG GAC CCG GCT GAG TTT GGC AAT GTC ACC TCC CTG CGC GTC CCT TCA GAG ATG
 210
 Glu Trp Asn Asp Tyr Lys Leu Arg Trp Asp Pro Ala Glu Phe Gly Asn Val Thr Ser Leu Arg Val Pro Ser Glu Met
 70
 80

FIG. 18A

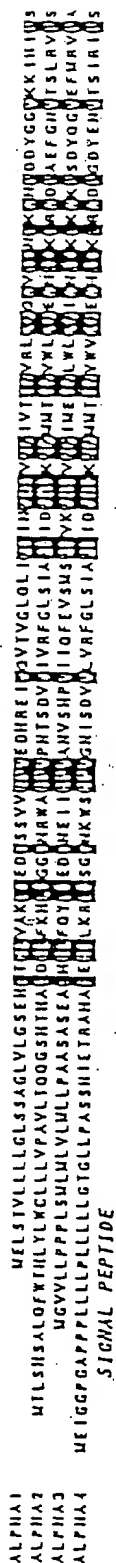
270 ATC TGG ATC CCA GAC ATT GTC CTC TAC AAC AA gtaaga.....ctcttccag T 300
 90 ile trp ile Pro Asp ile Val Val Leu Tyr Asn As 100
 330 ACC ATG Met 110
 360 GCT CAC CTC TTC TTC ACG GGC ACT GTG CAC TGG GTG CCC CCA GCC ATC TAC 390
 120 Ala His Leu Phe Phe Thr Gly Thr Val His Trp Val Pro Pro Ala ile Tyr 130
 420 CCC TTC Phe Pro Phe 140
 450 GAC CAG CAG AAC TGC AAG ATG AAG TTT GGC TCC TGG ACA TAT GAC AAG GCC 480
 150 Asp Gln Gln Asn Cys Lys Met 160
 510 GAC CTG Val Asp Leu 170
 540 AAG GAC TAC TGG GAG AGT GGC GAG TGG GGC ATT ATC AAT GCC ACC GGA ACC 570
 180 Lys Asp Tyr Trp Glu Ser Gly Glu Trp Ala ile ile Asn Ala Thr Gly Thr 190
 600 ATC TAC ile Tyr 200
 630 CCC GAT GTC ACC TAC TTT TTT TTT GCG GTG ACC CAC TAT GCG GTG GAG AGG ACA 660
 210 Pro Asp Val Thr Tyr Tyr Phe 220
 690 TCC Ser Cys Leu 230
 720 ACT GTG CTC GTG TTC TAC CTG CCT Pro 240
 750 TCC GAG TGT GGA GAG AAG ATC ACG CTG TGC ATC TCG GTG CTG CTA TCT CTC ACT GTC 780
 250 Thr Val Leu Val Phe Tyr Leu 260
 810 CTC ATC ACG GAG ATC ATC CCG TCC ACC TCG CTG GTC ATC CCA CTC ATC ATG ATC TTT GTC 840
 270 Leu ile Thr Glu ile ile Pro 280
 870 CTC TCT Thr Leu Ser 290

FIG. 18B



ATC GTT ATC ACA GTC TTC GTG 900 AAT GTA CAC CAC CGC TGC CCC AGC ACC 930 AAC ATG CCC AAC TGG GTA AGG GTA GCC CTA GGC
11e Val 11e Thr Val Phe Val 300 Leu Asn Val 11s 11s Arg Ser Pro Ser Thr 310 His 310 Leu Val 11e 320 Leu GGC
CGG GTG CCC AGG TGG CTG ATG ATG AAC CGG CCC CTG CCA CCT ATG GAG CTC CAT 1020 GGC TCC CCG GAT CTG AAG CTC AGC CCC TCA TAC CAT
Arg Val Pro Arg Trp Leu Met 330 Met Asn Arg Pro Leu Pro Pro Met Glu Leu 340 His 340 Ser Pro Asp Leu Lys Leu Ser Pro Ser Tyr 11s
TGG CTA GAG ACT AAC ATG GAT GCT GGA GAA AGG GAG GAG ACA GAG GAA GAG GAA GAA GAT GAA AAC ATA TGT GTG TGT GCA GGC
Trp Leu Glu Thr Asn Met Asp 360 Ala Gln Glu Arg Glu Glu Thr Glu Glu Glu Glu Asp Glu Asn 11e Cys Val Cys Ala Gly 380
CTT CCA GAC TCT TCG ATG GGT GTC 1170 CTC TAT GGC CAT GGC GGC CTG CAT CTG AGA GGC ATG GAG CCT GAG ACC AAG ACT CCA TCC CAG GCT
Leu Pro Asp Ser Ser Met Gly 390 Leu Tyr Gln 11s Gly Gly Leu His 400 Ala Met Glu Pro Glu Thr Lys Thr Pro Ser Gln Ala 410
AGC GAG ATT CTG CTG TCA CCT CAA 1260 ATA CAG AAA GCA CTA GAA GGT GTA CAC TAC ATT GCT GAC CGT CTG AGG TCT GAG GAT GCT GAC TCT
Ser Glu 11e Leu Leu Ser Pro 420 Gln 11e Gln Lys Ala Leu Glu Gly Val His 430 Tyr 11e Ala Asp Arg Leu Arg Ser Glu Asp Ala Asp Ser 440
TCG gtgaagt.....ctaacttcag 1350 GTG AAG GAA GAC TGG AAG TAT GTG GCC ATG GTG GTA GAC CGG ATA TTC CTC TGG CTG TTC ATT ATC
Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val Val Asp Arg 11e Phe 460
GTC TCG TTC CTG GGG ACC ATC GGA CTC TTC CTT CCT CCA TTC CTG GCT GGA ATG ATC TAA CTTCATGTCCTTCATGTTGGCTCCMAGGTGGCCTTCGTA
Val Cys Phe Leu Gly Thr 11e Gly Leu Phe Leu Pro Pro Phe Leu Ala Gly Met 11e 470
1410
1500 ACTATCTCTAGTCTTCTGTGMAATGGAGCCATCTCTAGMATACCTCTTTGAC.....3'

FIG. 18C

[illegible]

ALPHA1
ALPHA2
ALPHA3
ALPHA4

01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038

[illegible]

ALPHA1
ALPHA2
ALPHA3
ALPHA4

RSLVQHVPSSQEALEDGIRCSRHS IOYCVSOGGAASLADSKPTSPISLKARPSQLAVSDOASPCKCTCKEAPSPVSPVTVLXAGGTAKPQHLPLSLATRVVEGDTPKSHILKXE
CYTOPLASMIC REGION

SPLIKHNEVKSMTEGTHRETUKSO
SEILLSIOIOKALEGHIAORLRSE
SLALSLSDEIKETOSKREIHUKAO

AMPHIPHATIC HELIX

[illegible]

FIG. 20A

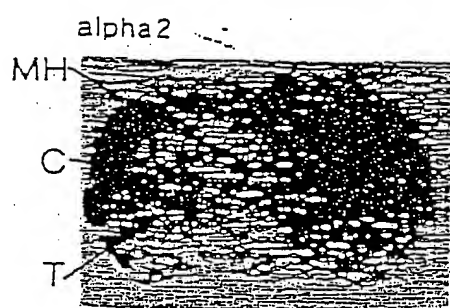
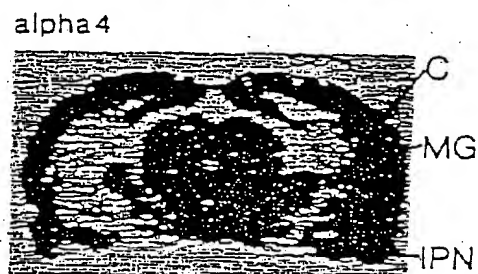
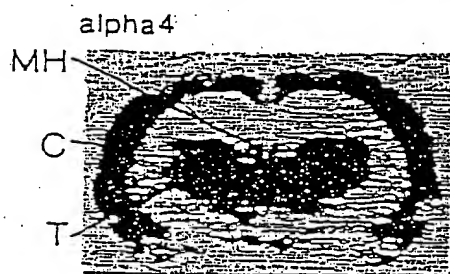
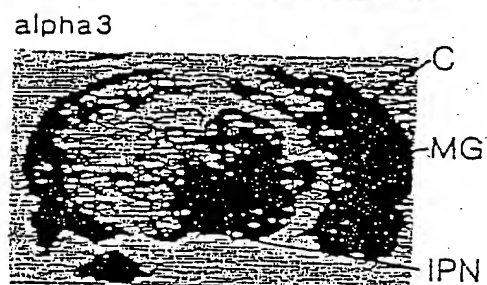
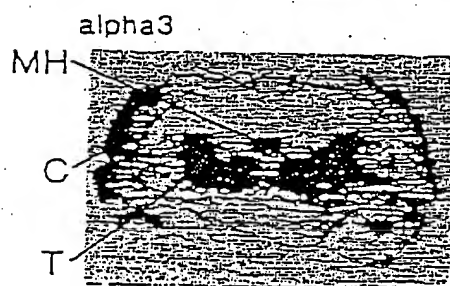
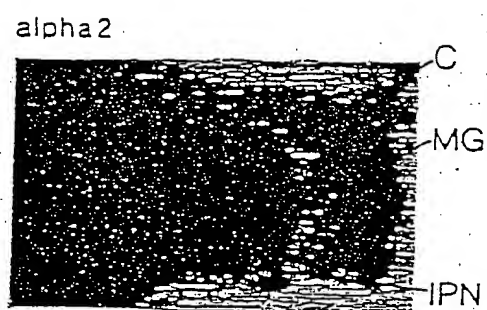


FIG. 20B



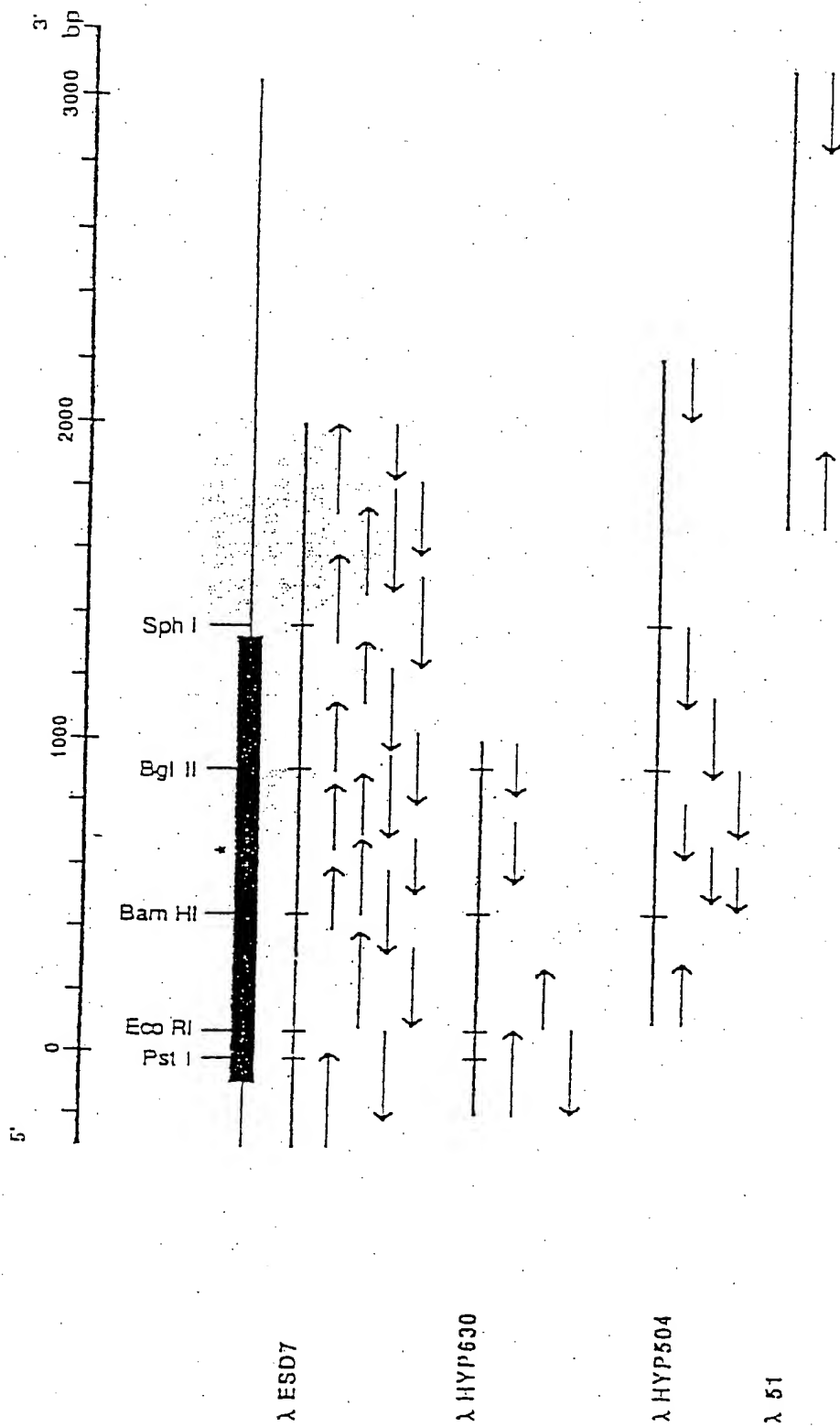
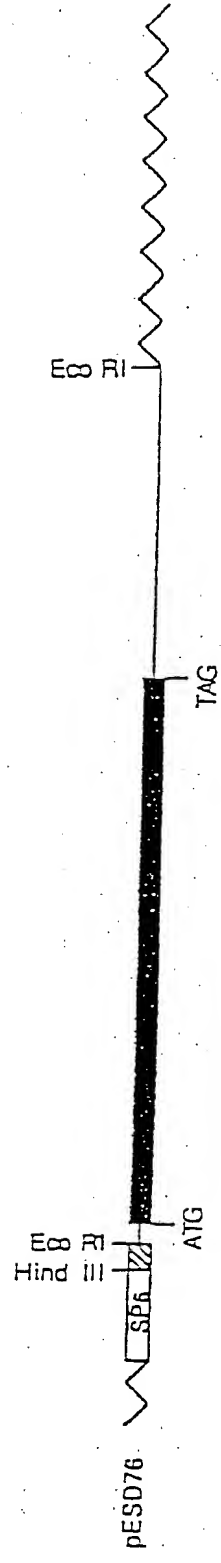


FIG. 21A





5'CACAGACATT
-240
TGTGCTCATCAGCTGATTATTTTCATCAGGCAGCTGGTCAGGTCCTGGTTTCATCAGGCTTTGAACCACTCACATTTTGTGTTTAAACCTGATCTTTCCAGTGGAAACACT
-220
-180
-160
-140
CTGCGCTTCAAGAAATGTCCTCTCAAGCAGACGTC ATG ACA GGC TTC CTA AGG GTC TTC TTG GTT CTC AGT GCC ACT CTC TCA GGT TCC TGG GTG
-120
-100
-80
-60
-40
Met Thr Gly Phe Leu Arg Val Phe Leu Val Leu Ser Ala Thr Leu Ser Gly Ser Trp Val
-30
-20
-10
Thr Leu Thr Ala Thr Ala Gly Leu Ser Ser Val Ala Glu His Glu Asp Ala Leu Leu Arg His Leu Phe Gln Gly Tyr Gln Lys Trp Val
ACT CTT ACG GCC ACT GCA GGA CTC AGC TCA GTG GCT GAA CAC GAA GAC GCA CTC CTC AGA CAT TTG TTC CAA GGT TAC CAG AAA TGG GTC
-20
-1
-1
30
Arg Pro Val Leu Asn Ser Ser Asp Ile Ile Lys Val Tyr Phe Gly Leu Lys Ile Ser Gln Leu Val Asp Val Asp Glu Lys Asn Gln Leu
CGC CCT GTG TTG AAT TCC AGT GAC ATC ATA AAA GTG TAT TTT GGA TTA AAA ATA TCC CAG CTT GTG GAT GAA AAG AAT CAG CTG
80
100
120
140
160
Met Thr Thr Asn Val Trp Leu Lys Gln Glu Trp Thr Asp Gln Lys Leu Arg Trp Asn Pro Glu Glu Tyr Gly Gly Ile Asn Ser Ile Lys
ATG ACG ACA AAT GTG TCG CTC MAG CAG GAA TGG ACA GAC CAA AAA TTA CGC TGG AAT CCG GAA GAA TAT GGT GCA ATT AAT TCG ATA AAG
180
200
220
240
90
Val Pro Ser Glu Ser Leu Trp Leu Pro Asp Ile Val Leu Phe Glu Asn Ala Asp Gly Arg Phe Glu Gly Ser Leu Met Thr Lys Ala Ile
GTT CCA TCA GAA TCG CTC TGG CTC CCG GAC ATA GTT CTC TTT GAA AAT GCT GAC GGA CGT TTT GAG GGC TCC CTC ATG ACC AAG GCC ATT
260
280
300
320
110
120
130
140
Val Lys Ser Ser Gly Thr Val Ser Trp Thr Pro Pro Ala Ser Tyr Lys Ser Ser Cys Thr Met Asp Val Thr Phe Pro Phe Asp Arg
GTG AAG TCC AGT GGA ACC GTC AGC TGG ACT CCT CCC GCC AGC TAC MAG AGT TCC TGC ACC ATG GAT GTC ACA TTT TTC CCG TTC GAG AGG
340
360
380
400
420

FIG. 22A



150
Gln Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Thr Met Val Asp Leu Ile 160
CAG AAC TGC TCG ATG AAG TTT GGA TCC TGG ACT TAC GAC GGT ACC ATG GGT GAC CTC ATT CTA ATC AAT GAA AAC GAT GGT GAC CGG AAA GAC 170
440 " 460 500

180
Phe Phe Asp Asn Gly Glu Trp Glu Ile Leu Asn Ala Lys Gly Met Lys Gly Asn Arg Arg Glu Gly Phe Tyr Ser Tyr Pro Phe Val Thr 200
TTT TTT GAT AAC GGA GAG TGG GAG ATA CTC AAC GCA AAG GGG ATG AAG GGC AAC AGA GAA GGC TTT TAC TCC TAT CCG TTT GTT ACC
520 540 560 580 600

210
Tyr Ser Phe Val Leu Arg Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Leu Gly Leu Ser Phe Leu Thr Val Leu Val 230
TAC TCT TTT GTC CTG ACA CGC CTG CCC TTG TTT TAC AGC CTC TTT TTG ATA ATC CCC TGC CTG GGG TTG TCT TTT CTC ACG GTC CTG GTG
620 640 660 680

240
Phe Tyr Leu Pro Ser Asp Glu Gly Glu Lys Leu Ser Leu Ser Thr Ser Val Leu Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu 260
TTC TAC CTA CCC TCG GAC GAA GGG GAA AAA CTC TCA TTA TCC ACC TCC GGT TTG GTC TCT TTG ACG GTG TTT CTT TTA GTG ATT GAA GAA
700 720 740 760

270
Ile Ile Pro Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met Ile Phe Val Thr Leu Ser Ile Ile Val Thr 290
ATA ATC CCG TCC TCT TCG AAG GTC ATC CCC CTC ATT GGC GAG TAC CTC CTC Tyr Leu Ser Ile Ile Val Thr 800 820 840 860

300
Val Phe Val Ile Asn Val His His Arg Ser Ser Ser Thr Tyr His Pro Met Ala Pro Trp Val Lys Arg Leu Phe Leu Gln Arg Leu Pro 320
GTT TTT GTA ATT AAT GTC CAC CAC AGA TCT TCC TCC TCA ACG TAC CAT CCC ATG GCC CCC TGG GTG AAG AGG CTG TTT CTA CAA AGA CTC CCG
880 900 920 940 960

330
Arg Trp Leu Cys Met Lys Asp Pro Met Asp Arg Phe Ser Phe Pro Asp Gly Lys Glu Ser Asp Thr Ala Val Arg Gly Lys Val Ser Gly 350
AGA TGG CTT TGC ATG AAG GAC CCC ATG GAC CGC TTC TCT TTC CCG GAT GGA AAG CAG AGT GAT ACA GCC GTG AGG GGG AAA GTC TCA GGC
980 1000 1020 1040

FIG. 22B



Lys Arg Lys Gln Thr Pro Ala Ser Asp Gly Glu Arg Val Leu Val Ala Phe Leu Glu Lys Ala Ser Glu Ser Ile Arg Tyr Ile Ser Arg
AAA AGG AAA CAG ACT CCC GCC AGC GAT GGA GAA AGA GTT CTG GTC GCT TTC CTC CAG AAG GCC TCC GAG TCC ATC AGA TAC ATT TCG AGG
1060 1100 1120 1140

His Val Lys Lys Glu His Phe Ile Ser Gln Val Val Gln Asp Trp Lys Phe Val Ala Gln Val Leu Asp Arg Ile Phe Leu Trp Leu Phe
CAT GTG AAA AAG GAA CAC TTC ATC AGC CAG GTA GTG CAA GAC TGG AAA TTT GTG GCT CAA GTT CTG GAC CGC ATC TTC CTG TGG CTC TTT
1160 1200 1220

Leu Ile Ala Ser Val Leu Glu Lys Ile Phe Ile Pro Ala Leu Lys Met Trp Ile His Arg Phe His
CTG ATA GCT TCT GTG TTG GGT TCC ATT CTG ATT TTT ATT CCA GCC TTG AAG ATG TGG ATA CAT CGT TTC CAC TAG GAGCCACTCTCTGGACCCA
1240 1300 1320

TTTAGAGACATACATAGAGACAAATCCCACTTAGGACTGACAGCGGCTGGCATGCTGACAGGAGCAGGCGCATGCTAGTGGTGGCCCTGTCTTGTCTGGAGCTTTCTGTG
1340 1360 1380 1400 1420 1440

ATTGCAGGGCACTGACAGAATGTGGGTTTGAGTTAGTGCAGATGGTGGCTGCCATTACAGGTGTAGTTGGGCAATTTGCGAGACGCTCTCCATGTTATTTATGTTGGGAGTTCTCTGAAC
1460 1480 1500 1520 1540 1560

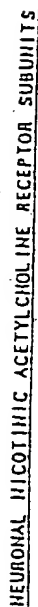
TACTCCCTCTGCTCATCCCTGCAAGCCACTGGGGCTATGTGCTATTTCTAGCAGTGTGGTCAAGCATTTTGACAAATAGTTTCAGGAAATTAGCGCAGGTACAACTCTCCACACACAGG
1580 1600 1620 1640 1660 1680

TCAAATTTCACACTGTGTCACAGGAGTGTCCACAAATAGGGTCAATTGAAGATGACCTTGAATGGCTATGACAGTCTCTPAAGGCAAGGTGTACTGGAAGTTTGTCTCACTGACCTGCGCAAC
1700 1720 1740 1760 1780 1800

TTTTTCAATGACAGGTAGGAACCTGGGCTGATTTCTAGCTTCTGTAGGTTCCATCAAAATAGTTTACCCCAAGAAACAGCCATTGGCTAGTACAACTGTATTATTACACACATCTC
1820 1840 1860 1880 1900

TTTTTTTTTCCC.....J'
1930

FIG. 22C



BETA 3
BETA 2
ALPHA 2
ALPHA 3
ALPHA 4
ALPHA 4

DETA 3	HSIKVPSLSL	QD	QI	IFENAD	QF	EGSL	TK	AL	VK	SS	GT	VS	WT	PP	AS	TJ	SS	TUD	YT	FP	TD	QI	NS	SK	GW	TD	GT	VL	QI	IL	HE	VON	K	D	F	DM	TWE	IL	AK	Q					
BETA 2	KKVL	PS	KH	QD	QI	YI	AD	QF	VS	FYS	I	AV	VS	DG	S	IF	AL	PP	AI	VS	CK	IE	VK	FP	TD	QI	NS	SK	GW	TD	GT	VL	QI	IL	HE	VON	K	D	F	DM	TWE	IL	AK	Q	
ALPHA 2	TS	LR	VP	SE	IM	QD	QI	YI	AD	QF	VS	TH	TK	AL	FT	GT	VL	QI	PP	AI	VS	SS	IS	DT	FP	TD	QI	NS	SK	GW	TD	GT	VL	QI	IL	HE	VON	K	D	F	DM	TWE	IL	AK	Q
ALPHA 3	EF	MR	W	AK	IM	QD	QI	YI	AD	QF	VS	DD	TK	AL	LY	GT	VL	QI	PP	AI	VS	SS	IS	DT	FP	TD	QI	NS	SK	GW	TD	GT	VL	QI	IL	HE	VON	K	D	F	DM	TWE	IL	AK	Q
ALPHA 4	TS	IR	DP	SE	IM	QD	QI	YI	AD	QF	VS	TH	TK	AL	FY	DG	RV	CT	PP	AI	VS	SS	IS	DT	FP	TD	QI	NS	SK	GW	TD	GT	VL	QI	IL	HE	VON	K	D	F	DM	TWE	IL	AK	Q

[illegible]

BETA 3
 BETA 2
 ALPHA 2
 ALPHA 3
 ALPHA 4

ALPHA 4
PLEVPOLKLTSEVEKASPCSPGSECPPPKSSGAPULIKANSLSVOHVP55OEAAEDGIRCRNRSLIOYCVSODGAASLADSKTSSPTSLKARPSOLPV5SDASPCXCT
-----CYTOTOXIC REGION-----

[illegible]

FIG. 23

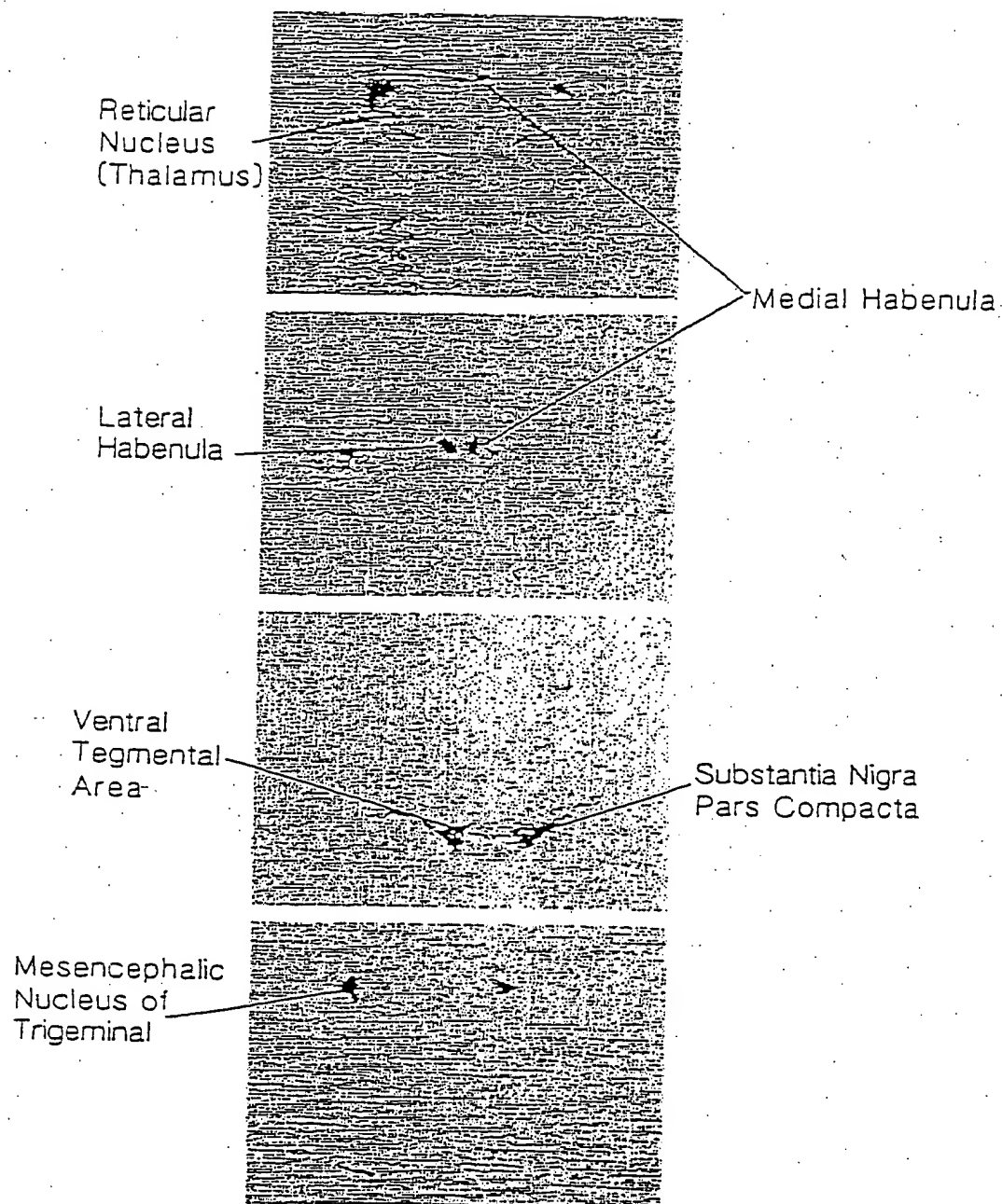


FIG. 24



FIG. 25

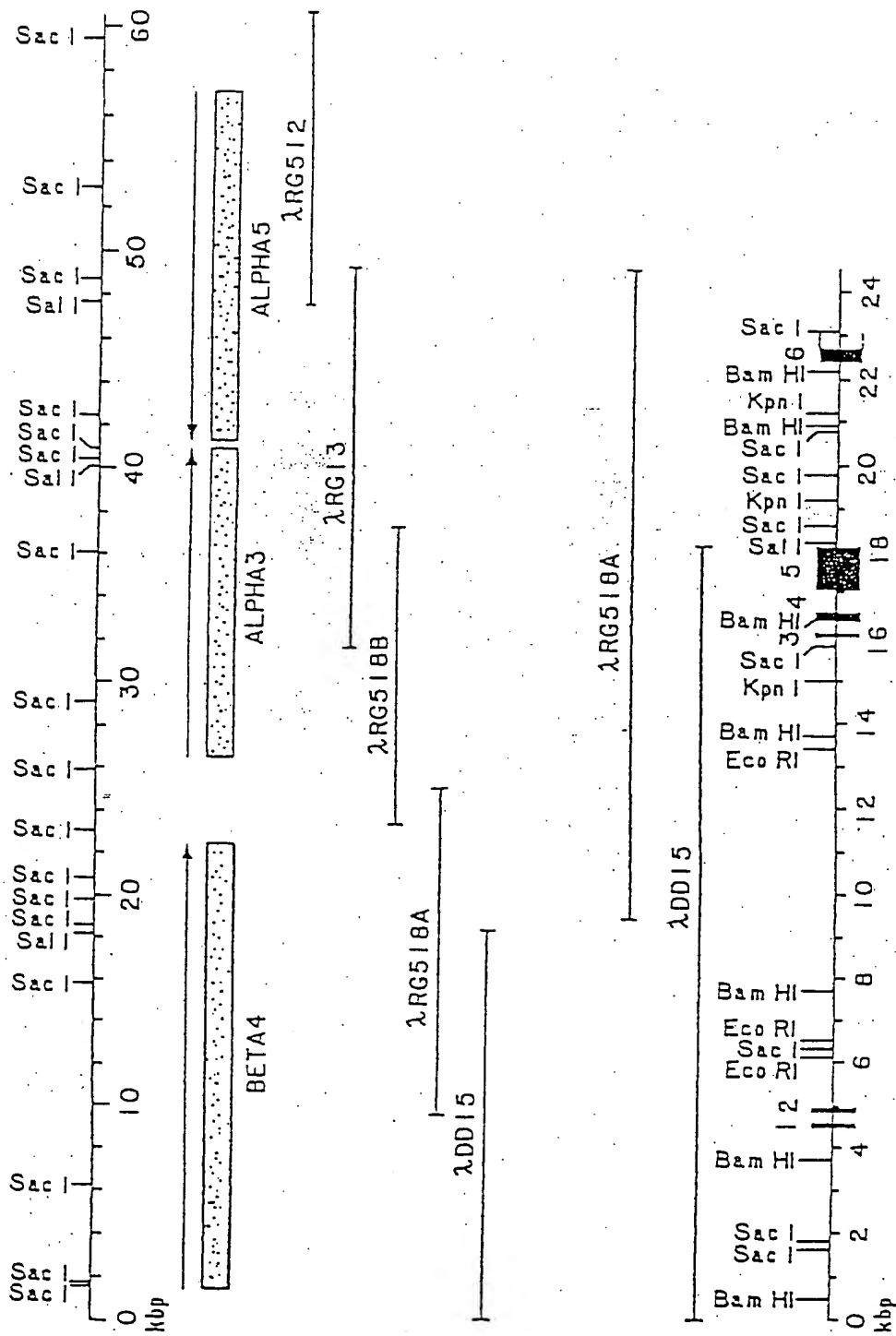


FIG. 26



5'...GCCAACCGGACAT
-120

ACGCTCACTCGCGGTTTCATTTAGTAGTGACCGGCTGACACCGGCTGCGC
-100

Met Arg Gly Thr Pro Leu Leu Leu Val Ser Leu Phe Ser Leu Leu Gln Asp
-10
ATG AGG GGT ACG CCC CTG CTC GTC TCT TCT CTG TCT CTG CTT CAG GAC
-20

Gly Asp Cys Arg Leu Ala Asn Ala Glu Glu Lys Leu Het Asp Asp Leu Leu Asn Lys Thr Arg Tyr Asn Asn Leu Ile Arg Pro
-1
GGG GAC TGC CGC CTG GCC AAC GCA GAG GAG AAG CTG ATG GAT GAC CTC AAG AAA ACC CGG TAC AAC AAC CTG ATC CGC CCA
-20

Ala Thr Ser Ser Ser Gln Leu Ile Ser Ile Arg Leu Glu Leu Ser Gln Leu Ile Ser Val
30
GCC ACC AGC TCC TCT CAG CTC ATC TCC ATC CGC CTG GAG CTA TCA CTG TCC CAG CTC ATC AGT GTG
100

Arg Glu Gln Ile Het Thr Thr Ser Ile Tyr Leu Lys Gln
50
CGA GAA CAG ATC ATG ACC ACC AGC ATC TGG CTG AAA CAG gtaagtgaact... cttaggatg GAA TGG ACT GAC TAC CGC CTG GCC TGG AAC
160 180 200

Ser Ser Cys Tyr Glu Gly Val Asn Ile Leu Arg Ile Pro Ala Lys Arg Val Trp Leu Pro Asp Ile Val Leu Tyr Asn As
80
AGC TCC TGC TAT GAA GGG GTG AAC ATT CTG AGG ATC CCC GCA AAG CGT GTC TGG TTG CCT GAC ATC GTC TTG TAC AAC AA gtagtgaca...
220 240 260 280

...cctaccacag T GCC GAT GGC ACC TAT GAG GTG TCT GTC TAC ACC AAC GTG ATT GTG CGT TCC AAC GGC AGC ATC CAG TGG CTG CCC CCT
100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360

FIG. 27A



Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp 140
GCT ATC TAC AAG AGT GCC TGC TGC AAG ATT GAG GTG AAG CAC TTT CCC TTC GAC CAG CAG AAC TGC ACC CTC AAA TTC CGC TCC TGG ACC TAT 130
380 400 440

Asp His Thr Glu Ile Asp Met Val Leu Lys Ser Ala Thr Ala Ile Met Asp 170
GAC CAC ACG GAG ATT GAC ATG GTT CTT AAG TCG CCC ACG GCC ATC ATG GAT GAC TTC ACC CCC AGT GGT GAA TGG GAC Ile Val Ala Leu 180
480 500 520 540

Pro Gly Arg Arg Thr Val Asn Pro Gln Asp Pro Ser Tyr Val Asp Val Thr 200
CCA GGA CGG AGG ACG GTG AAC CCT CAG GAC CCC AGC TAC GTG GAC GTG ACC TAT GAC TTC ATC ATC AAG CGC AAC GCG CTC TTC TAC ACC 210
560 580 600 620

Ile Asn Leu Ile Ile Pro Cys Val Leu Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys 240
ATC AAT CTT ATC ATT CCT TGT GTG CTC ATC ACC TCG CTG GCT ATC ATC CTG GTC TTC TAC CTG CCC TCC GAC TGT GGG GAG Ile Met Thr Leu 230
640 660 680 700 720

Cys Ile Ser Val Leu Leu Ala Leu Thr Phe Phe Leu Leu Leu Ile Ser Lys Ile Val Pro Pro Thr Ser Leu Asp Ile Pro Leu Ile Gly 270
TGC ATC TCT GTG CTG CTG GCA CTC ACG TTC TTC CTG CTG CTC ATC ATC TCC AAG ATC GTG CCT CCC ACC TCC CTT GAC ATA CCG CTC ATT GGC 260
740 760 780 800

Lys Tyr Leu Leu Phe Thr Met Val Leu Val Thr Phe Ser Ile Val Thr Thr Thr Val Cys Val Leu Asn Val His His Arg Ser Pro Ser Thr 300
AAG TAC CTC TTG TTC ACC ATG Val Leu Val Thr Phe Ser Ile Val Thr Thr Thr Val Cys Val Leu Asn Val His His Arg Ser Pro Ser Thr 290
840 860 880 900

His Thr Met Ala Ser Trp Val Lys Glu Cys Phe Leu His Lys Leu Pro Thr Phe Leu Phe Met Lys Arg Pro Gly Leu Glu Val Ser Leu 330
CAC ACC ATG GCA TCC TGG GTC AAG GAG TGC TTC CTG CAC AAA CTG CCC ACC TTC CTC TTC ATG AAG CGT CCC GGT CTT GAA GTC AGC CTG 320
920 940 960 980

FIG. 27B



340
Val Arg Val Pro His Pro Ser Gln Leu His Leu Ala Thr Ala Asp Thr Ala Ala Thr Ser Ala Leu Gly Pro Thr Ser Pro Ser Asn Leu
360
370
Tyr Gly Ser Ser Met Tyr Phe Val Asn Pro Val Pro Ala Ala Pro Lys Ser Ala Val Ser Ser His Thr Ala Gly Leu Pro Arg Asp Ala
390
TAT GGG AGT TCC ATG TAC TTT GTG AAC CCT GTC CCT GCC CCT AAG TCT GCA GTC ACC TCC CAC ACA GCA GGC CTC CCC AGG GAT GCC
1100
1120
1140
1160
1180
1200
Arg Leu Arg Ser Ser Gly Arg Phe Arg Glu Asp Leu Gln Glu Ala Leu Glu Gly Val Ser Phe Ile Ala Gln His Leu Glu Ser Asp Asp
420
CGT CTC AGG TCC TCC GGG AGG TTC CCG GAA GAT CTA CAG GAA GCA TTA GAG GGT GTC AGC TTC ATC GCC CAG CAT CTG GAC AGC GAT GAC
1240
1260
Arg Asp Gln Ser
CGA GAT CAA AGT gtatgtcactg... Val Ile Glu Asp Tyr Lys Phe Val Ala Met Val Val Asp Arg Leu Phe Leu Trp
430
440
450
Val Phe Val Phe Val Cys Ile Leu Gly Thr Met Gly Leu Phe Leu Pro Pro Leu Phe Gln Ile His Ala Pro Ser Lys Asp Ser
460
GTG TTC GTG TTT GTG TGT ATT CTG GGC ACC ATG GGG CTC TTC CTG CCA CCC GTT TTC CAG ATC CAC GCA CCC TCC AAG GAC TCC TAG GCT
1340
1360
1380
1400
1420
ACCCGGCITGTCGGGHHCCGGGAAAGTAGTGATGATATGAGAACGGGTGGGAGCAGCGGGTGTCTTTGGGCTACCCGGGCTGTCTCGGGCCCGGGGAAAGTAGTGATGATATGA
1440
1460
1480
1500
1520
GAAAGCGGTGGGAAAGCAGGGCGTGTCTTCGG...J'
1540

FIG. 27C

[illegible]

FIG. 28A



220 Phe Leu Ile Ile Pro Cys Ile Gly 230 Leu Pro Ser Asn Glu Gly Glu Lys Ile 240 Leu Cys
TTC CTT ATT ATC CCC TCC ATT GGG 700 TCA CCT TCA AAC GAG GGT GAA AAG ATT AGC CTC TGC
640 660 680

250 Thr Ser Val Leu Val Ser Leu Thr Phe Leu Val Val Val Thr Leu Thr Phe 260 Pro Ser Ser Ser Lys Val Ile Pro Leu Ile Gly Glu
ACC TCA GTG CTC GTC TCT CTC ACT TTC TTC GTC ATC GAG GAG GAT GTC ATA CCC CTG ATT GGG GAG
740 760 780 800

280 Tyr Leu Val Val Phe Thr Met Ile Phe 290 Phe Ala Ile Asn Ile His His Arg Ser Ser 300 Thr His
TAC TTG GTG TTC ACC ATG ATT TTC 820 Val Thr Leu Ser Ile Met Val Thr Val Thr Val GTC TTT GCC ATC AAC ATC CAC CAC CTC TCT TCC
840 860 880 900

310 Asn Ala Met Ala Pro Trp Val Arg 320 Leu Cys Met Arg Ser His Ala Asp Arg Tyr Phe Thr
AAC GCT ATG GCG CCC TGG GTT CGT AAG ATA TTT CTC CAC AAC CTT CCC AAG CTC TGC ATG AGA AGT CAT GCG GAT AGG TAC TTC ACT
920 940 960 980

340 Gln Arg Glu Glu Ala Glu Ser Gly 350 Ala Ala Leu Asp Cys Ile Arg Tyr Ile Thr Arg His
CAG AGA GAA GAA GCC GAG AGT GGG GCT GGA CCT AAA TCT CAC AAA TCT CAC AAC ACT TTG GAA GCC GCA CTC GAT TGC ATT CGC TAC ATC ACG AGG CAC
1000 1020 1040 1060 1080

370 Val Val Lys Glu Asn Asp Val Arg 380 Gln Val Leu Asp Arg Met Phe Leu Trp Thr Phe Leu
GTC GTG AAA GAG AAC GAC GTC CGC GAG GTT GTT GAA GAT TGG AAA TTC ATA GCC CAA GTC CTT GAT CGG ATG TTT TTG TGG ACG TTT CTT
1100 1120 1140 1160 1180

400 Leu Val Ser Ile Ile Gly Thr 410 Gly Leu Phe Val Pro Val Ile Ile Val Pro Val His Ile Gly Asn Thr
CTG GTG TCA ATC ATT GGG ACT TTA GGG CTT TTT GTT CCT GTT ATT TAT AAA TGG GCC AAT ATA ATA GTC CCA GTT CAC ATT GGA AAC ACA
1200 1220 1240 1260

FIG. 28B

ile Lys
ATT AAG TGA ACCAAGAAATTACCCGTGGGATTAGTGAGCAGTCATGCAGCCTCTTAGGACATGATGCTGTTATGGAAATGTGAAGGTAGTTACAATTTGACATAGGCTATAACA
1280 1300 1320 1340 1360 1380
GATTAGCAATTTCCTAACATTGGCTTAATGTTGTCCATTAGAACTGCAGTAATAACCTCAAAATAGCAACAACACATTTGTCTGCCTGCACTAGTAAGGGCCCTAGCATCTGCATCTCTGGCAA
1400 1420 1440 1460 1480 1500
ACCTTACCAATTTGCAACCAATGATGAAGGCCATCCTCTGGAGTGCTGGAAACTCAACTGTATTTGAAGACTATTTAAAACTCCCCCAAAATTTAGTAGGAACATATATATGTGTGGTT
1520 1540 1560 1580 1600 1620
TTGAATTTTCAGAAATGGGTCTTTGGGCTCTTGTAAATTTGTCTGGGTAGCACAAAACCTCTCTGAGTAGCTGGGACCATTGGGTGCTGCTGCACCTTTGCCCTGTTCTGTATTTCACAGATATA
1640 1660 1680 1700 1720 1740
AATACATCATTAATTTATAGGAGGTAGGCCCATTTACTTGGTTTAATAATAACTTAATTAATTAAGCTTAATGTCAGCTAAATGTTCTATTTGCTGTGAAGAGACATC
1760 1780 1800 1820 1840 1860
ATGACCAATCAACTCTTATAAAGAAACATTTTCATCAGTGTCTGGCTTACAGTTTTTTGAGGTTTAGCCAAATATATCAGAGTGAAGCATGATAGCATCCAGGTAGACATTAATGCTGGATCC
1880 1900 1920 1940 1960 1980
AGGAGTTCTCTACATCTGGAATCAGCAGGACAGCAGGAGAGAGCCACTGGACCTGGCTTGAGCATCTGAAACCTCAAAAGCCCACTCCAGTGACACACACTTCCCCCAACAAAGCCC
2000 2020 2040 2060 2080 2100
ACACTCTCTAATAGTGCCACTTGGCTGGTGATCAAGCATTCAGTCTATGGGTCTACGAGAGCCATTCTCTATTCAAACACACACTTAATAGGATGCTATTTCTTACTGACATTTTTTAATAAG
2120 2140 2160 2180 2200 2220
CGACAAATGGTAACTAGAACAATCTGTAGGCCACTTTACTCTTTATATGGTAATATGGATTGGCTTTATATTAATACTAGTTTTTACAGCCTATCTGAAACACATGTAACAGGCAACTCTCTG
2240 2260 2280 2300 2320 2340
CAGACACATTCCTTTGTAATGACTTTATATCTGCTGAGTGGCACTCTGCTGAGTCCACACTCTCGGGTTAGTAGAGCCATTATATGTACATCGCGGTATCCCTG
2360 2380 2400 2420 2440 2460
ATTTCAGAGCAACTGTGCAGTTGCACAGGTTCCCACTCAAAATGGGATGCCATGCTGTGGATAATTCCTGTGGAAACCACTTCTGAGCTGGATACGGTGCCTCATACCTGTCA
2480 2500 2520 2540 2560 2580
TGTCTACTTTTCAGAGGCGAGGCGAGGGGAATTCGTGTGAGTTGTTGGTTCAGCCCTGGGTTACATATGAGACCCCTGCTCTCAGAAACCAAAACAACTTCCCTGTGAGTTGATATAAG
2600 2620 2640 2660 2680 2700
CACACTGTCTATATCCGAATTTGGGATTCCTCTAGAGTCGACCTGACGGCATGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCG
2720 2740 2760 2780 2800

FIG. 28C



BITA2 HLACHAGHSHALFSLLMLCSGVLGTDEERLVEHLLDPBRYHKLIRPATNGSELVTQVHVSQAQLISVHEREQIMHTTHVHLTOEWEDEYHLTWKPEDFDHHK
BITA3 HTGFLRVFLVLSATLSGSWVLTATAGLSSVAEHEDALLRHLTQGYQKVPVPLNSSDIKVYGLKISQLVDVDEKHQLHTTHVHLKQEHTDOKLHHPEEYGGIH
BITA4 HRGTFLLLVSLFSLLOQGDCLAHAEKCLMDLLHMKTRYHNLIRPATSSQLISIRLELSQLISVHEREQIMHTTHVHLKQEHTDOKLHHPEEYGGIH
----- SIGNAL PEPTIDE -----

BITA2 KVLPLSKHMLPDPVLYHHADGHVEVSFYSHAVSYDGSIFHLPPAIYKSACKIEVHHFPGDQOHCCTHKFRSHTYDTEIDLVLKSDVASLDOFTPSGEMOIIALPG
BITA3 SIKVPSSESLHLPDIVLFENADGHEGSLMTKAIIVKSSGTVSWTPPASYSKSSCTHDVTFPPDRQHCSHKFGSMTYDGTHTVDLILTHEINORKDITFONGEWEILHANG
BITA4 ILRIPAKRWLPDIVLYHHADGHVEVSFYTHIVRSNGSIOMLPPAIYKSACKIEVHHFPGDQOHCCTHKFRSHTYDTEIDLVLKSDVASLDOFTPSGEMOIIALPG

BITA2 RMENHPDS TYVOITYDGIIRKPLFYTHLITPCVLITSALILVFLYLPSCDGEKHTLCISVLLALTIVFLLLISKIVPPTSLDVLVGVKYLHFTHVLTFSIVTSV
BITA3 HKGHRREGTYSYFVTVSYFVLRNLPLFYTLFLIIPCLGLSFLTVLVFLYLPSCDGEKHTLCISVLLALTIVFLLLISKIVPPTSLDVLVGVKYLHFTHVLTFSIVTSV
BITA4 RRTVUPDP SYDVTYDGIIRKPLFYTHLITPCVLITSALILVFLYLPSCDGEKHTLCISVLLALTIVFLLLISKIVPPTSLDVLVGVKYLHFTHVLTFSIVTSV
----- MSR I ----- MSR II ----- MSR III -----

BITA2 CVLHVHHRSPPT HTHAPWVUVVFLKPLTLLTLOQPRHRCARQLRLRRQRERECEAVTFREGPAADPCSVGPCSCG
BITA3 FVIVHHRSSSTYBPHAPWVUVVFLKPLTLLTLOQPRHRCARQLRLRRQRERECEAVTFREGPAADPCSVGPCSCG
BITA4 CVLHVHHRSPST HTHASHVNECFHLKPLTLLTLOQPRHRCARQLRLRRQRERECEAVTFREGPAADPCSVGPCSCG

BITA2 LREAVDGVRFIADHHRSEDDQSVREDKXYVAHVDRFLFLNIFVFCVGTGVLQPLQHYTATTLHPDHSAPSSK*
BITA3 ASESTYISNVKKEHFIQVQVQDQKFGVAVQVLDRIFLFLIASVLGSLIFIPALKHNRHF*
BITA4 SGFRFREDQEALEGVSFIAQNLSDQDQSVIEDKXFAHVQVDRFLFLNIFVFCVGTGVLQPLQHYTATTLHPDHSAPSSK*
----- MSR IV -----

FIG. 29

ALPHA2 HTLSHALQFMTILYLHCLLLVPAVLTOQGSHTHAEDRLFKHLTGGYHNRHARVPVPHTSDDVIVRGLSIAQLIDVDEKIQHMTTHVHLKQEHNOYKLRWOPAE
 ALPHA3 HGVVLLPFPPLSHLHLVHLHLLPAAASASEAHEHLFOYLFEDYNEIIRAPVAHVSHPVIIQFVSHSGLVXKVDEVIQIHETHLKQIWHYOYKLRWKPSP
 ALPHA4 HEIGGPGCAPFPLLLPLPLLLGLTGLLPASSHIEIETRAHAEEILLKRLFGSYHKSAPVGHISDVLVFRGLSIAQLIDVDEKIQHMTTHVHLKQEHNDYKLRWDPGD
 ALPHA5 HVQLLAGNRPTGARRGTAGGLPELSSAAXKHEDSLFRDLFPEDYERHVRPVEHLSQKIKINFGLAISQLVDVDEKIQHMTTHVHLKQEHNDVLRWHPDO
 _____ SIGNAL PEPTIDE _____

ALPHA2 FGHVTSLRVSEHIIPOIVLYNHADGEFAVTHHTKAHLFFTGTVHNVPPAIYKSSCSIDVTFPFDQOCHKHKTGSHTYDKAKIDLEQHMTVOLKDYHESGEWA
 ALPHA3 YOGVEFHRVPAEKIMKPOIVLYNHADGDFQVDDKTALLIKYTGVEVTHIPPAIKSSCKIDVTFPFDYONCTHKTGSHTYDKAKIDLVLGSSHLKDYHESGEWA
 ALPHA4 YEHVTSIRIPSELIHWPVLYNHADGDFAVTHHTKAHLFYDGRVQHTPPAIYKSSCSIDVTFPFDQOCHKHKTGSHTYDKAKIDLVSHSRVDQDFWESGEHV
 ALPHA5 YGGIKIIRVPSDSLHWPVLYNHADGDFEGAS TKTVVRYHGTVTHTQPAHYKSSCTIDVTFPFDQOCHKHKTGSHTYDKAKIDLVSHSRVDQDFWESGEHV

ALPHA2 IIHATGTYHNSKYDCCAEIYPDVTVYFVIRRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLLLITEIIPSTSLVPLIGEYLLFTTHIF
 ALPHA3 IIKAPGYKHEIKYHCCAEIYQDITVLSYIRRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLLLITEIIPSTSLVPLIGEYLLFTTHIF
 ALPHA4 IVDAGTYHTRKYHCCAEIYPOITYAFIIRRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLLLITEIIPSTSLVPLIGEYLLFTTHIF
 ALPHA5 IMSHSGKHRTDSCCH YPIITVSFVIKRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLLLITEIIPSTSLVPLIGEYLLFTTHIF
 _____ MSR I _____ MSR XI _____ MSR XII _____ MSR XIII

ALPHA2 VTLSIVITVFLVHVRSPSTHHPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGRETEEEEEEEEDENICVCAGLPDSSHCVLYG
 ALPHA3 VTLSIVITVFLVHVRSPSTHHPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGRETEEEEEEEEDENICVCAGLPDSSHCVLYG
 ALPHA4 VTLSIVITVFLVHVRSPSTHHPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGRETEEEEEEEEDENICVCAGLPDSSHCVLYG
 ALPHA5 VTLSIVITVFLVHVRSPSTHHPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGRETEEEEEEEEDENICVCAGLPDSSHCVLYG

ALPHA2 HGLHLRAHEPETKTPSOA
 ALPHA3 TRSSSESVMHVL
 ALPHA4 TCRSPLEVPDLATSEVENASPCBPBGSCPPPKSSGAPHILKARSLVQHVPSQEAEDGIRCSHNSIOYCVSODGAAASLADSKPTSSPTSLKARPSQLPV5DQ
 ALPHA5

ALPHA2 SKLLSPQIOKALEGVHYIADRLRSEDADSSVKEDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 ALPHA3 SLSALSPEIKAEIQSVKYIAEHKXQHVAKIEQDDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 ALPHA4 ASPCKGCTCKEPSVPSPVTVLKAGGTAKAPPQIPLSPALTRAVEGVQYIADHLKAEEDTFSVKEDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 ALPHA5 LEAALDCIRYITRHHVVKENDVREVEEDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 _____ MSR IV _____

FIG. 30

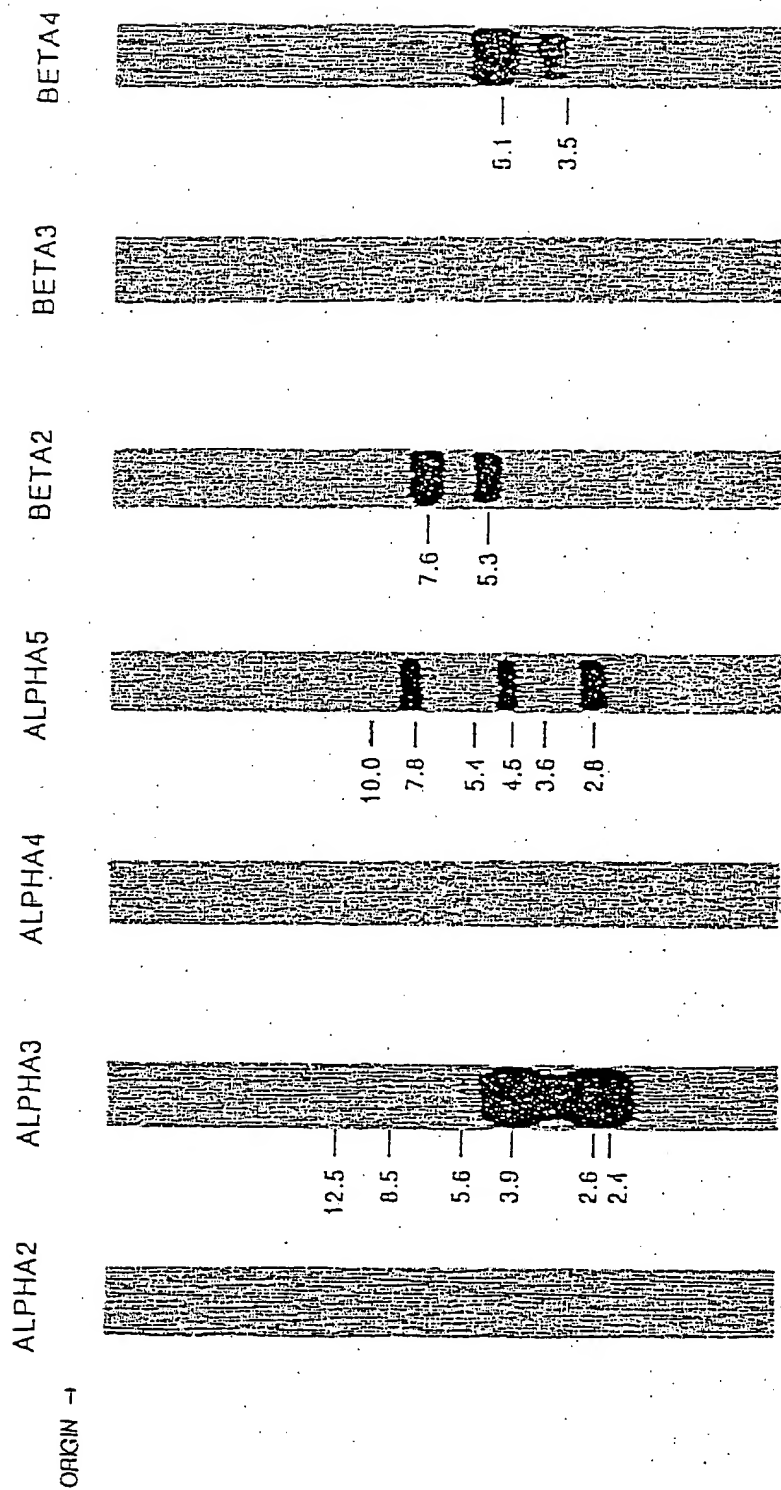


FIG. 31

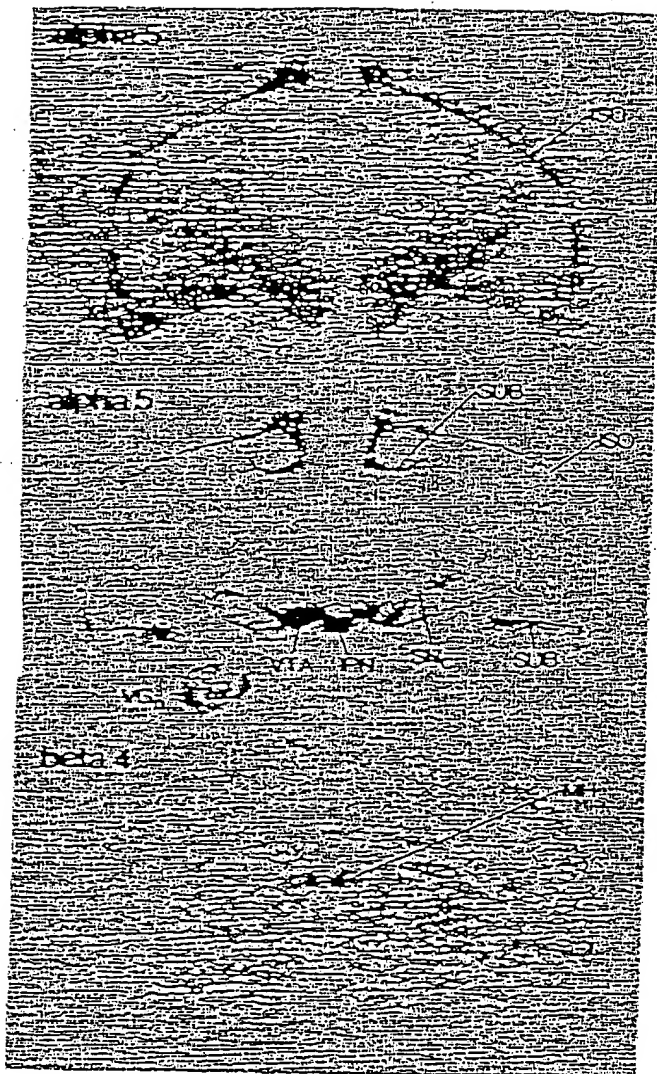


FIG. 32